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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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REFERENCE	JOURNAL	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	CGL17592	RESULT 1
2 (bases 1 to 2123)	Unpublished	Kim, K., Peters-Wendisch, P.G., Sahm, H. and Eikmanns, B.J.	P	Corynebacterineae; Corynebacteriaceae; Corynebacterium.	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	Corynebacterium glutamicum	Corynebacterium glutamicum	accDA gene; acetyl-CoA carboxylase; carboxyltransferase.	Y17592.1 GI:14572581	Y17592	Corynebacterium glutamicum accDA gene.	CGL17592 2123 bp DNA linear BCT 26-JUN-2001		

Qy Db	P &	DF Q	Db Qy	Db Qy	Qy Db	g <i>Q</i> y	B Q	Db Qy	Query Match Best Local Matches 212	BASE COUNT				CDS	gene		COMMENT FEATURES SOURC		AUTHORS
481 ATTAATTAACAAAGCCATTTTTCGGCCGTGGAGAAGCGTTTTCCGACTATGGTGTGGGGC 540 	421 TCGATAGCCTAAATTGGGCTTAGATCTTCCGCCTCTAAATAGGTATGCAGAGACATTCGA 480	361 ACGTCTAGGCAAAAAGTAGTTTTGTGAGATGAAACGCATAATCCGTCATTTTTTACGCAA 420 	301 GTGCAATAGTTAACGGGCTTCACACGTCACCATTCTGTCCGGTTTTAGGCTATGTTCGGG 360	241 TCCCGATCTACCCCCTCTTTACCCCGAAATACCCCTTTTGCAAAGATTGCAAACACAACA 300	181 ACTCCCCCAATATCTTAACTTAAACTTAAAAGTAGTGTTTTACCTGCATTTATAAAAGT 240 	121 AACGTGTGAAGTGAAGTTACCTAACTCACATTGCAATTGCGATAGCGATTTGGAAAACTC 180	61 CTTATATGTTTCTCACCACATCTGGCCGACGACGACGAAGTATGTTGTCGATCACAGCTA 120	1 CTCGAGCGGGAGTCGGTGATCGGCCACTCTCTAAGCAATGCCGGCTTTAAAATAAAGCAA 60 	100.0%; Score 2123; DB 1; Length 2123; al Similarity 100.0%; Pred. No. 0; 2123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	4	AMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSP LQLRAAVAKTLKVIQPVEATDRFSFTTPGVALPVMBALARSRDPQRPGIGEIWETLGA DVVKLSGARAGALSPAVRVALARIGGRPVVLIGQDRRFTLGPQELRFARRGISLAREL NLPIVSIIDTSGAELSQAAEELGIASSIARTLSKLIDAPLPTVSVIIGGGVGGGALAM	/db xref="GI:14572582" /db xref="GI:14572582" /db xref="GI:14572582" /translation="MEKRFPTMYWGMEHTSALTLIDSVLDPDSFISWNETPQYDNLNQ /translation="MEKRFPTMYWGMEHTSALTLIDSVLDPDSFISWNETPQYDNLNQ GYASTLERAAKAKCDESVLTGEGGTVEGIPVAVILSDPSFLGGSLGTVASVRIMKAIH RATELKJILVSPAGGGARMOEDNBAFVMYSITBANOFHFRAHI,PFLVYLNNDTMYG	/transI table=11 /transI table=11 /producT="putative carboxyltransferase subunit of acetyl-CoA carboxylase" /profun id="RAC42827 1"	5081983 /gene="accDA" /codon etart=1	/8f7aln="AfCC 13032" /db_xref="taxon:1718" 5081983 /gene="accDA"			Submitted (17-JUN-1998) P.G. Peters-Wendisch, University of California at Berkeley, Dept. Plant and Microbial Biology, Kustu Lab, 111 Koshland Hall, Berkeley CA 94720, USA	
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Query Match 100.0%; Score 2123; DB 6; Length 2123; Best Local Similarity 100.0%; Pred. No. 0; CTCGAGCGGGAGTCGGTGATCGGCCACTCTCTAAGCAATGCCGGCTTTAAAATAAAGCAA 60 1 CTCGAGCGGGAGTCGGTGATCGGCCACTCTCTAAGCAATGCCGGCTTTAAAATAAAGCAA 60 61 CTTATATGTTTCTCACCACATCTGGCCGACGAAGTATGTTGCGATCACAGCTA 120 61 CTTATATGTTTCTCACCACATCTGGCCGACGAAGTATGTTGCGATCACAGCTA 120 61 CTTATATGTTTCTCACCACATCTGGCCGACGAAGTATGTTGCAAAACTC 180 121 AACGTGTGAATGTGAAGTTACCTAACTCACATTGCAATGCGATTTGGAAAACTC 180 122 AACGTGTGAATGTGAAAGTTACCTAACTCACATTGCAATGCGATTTGGAAAACTC 180 Db Db Db Db Db Db Db DD DD D	Unknown. Unclassified. (bases 1 to 2123) (bases 1 to 2123) (bases 1 to 2123) (cost 1 to 2123) Process for the preparation of L-amino acids by fermentation and nucleotide sequences coding for the accDA gene Patent: US 6361986-A 1 26-MAR-2002; Location/Qualifiers 1. 2123 Jorganism="unknown" 460 a 574 c 592 g 497 t	2101 GCCGACCTTCATGCCTGGAATTC 2123 Db AR202319 AR202319 N AR202319 AR202319 AR202319 AR202319 AR202319 AR202319 AR202319.1 GI:20256858 Unknown.	AACAATCCGGAGAGGCGGACAGTCGCTTCACACACTTTTTTTT	1621 GCTCCCCTCCCCACCGTTTCGGTCATTATTGGTCAGGGGGTTGGCGGTGGCGCTTGGCC 1680 1621 GCTCCCCTCCCCACCGTTTCGGTCATTATTGGTCAGGGGGTTGGCGGTTGGCGCTTGGCC 1680 1681 ATGCTGCCCGCCGATCTGGTCTACGCGGCCGAAAACGGCGTTGGCGATTGCCACCA, 1740 1681 ATGCTGCCCGCCGATCTTGGTCTACGCGGCCGAAAACGGCGTGGCTGTCCGCATTGCCACCA, 1740 1741 GAGGGCGCCTCGGCCATCCTCTTCCGCGACACCAACCAAC
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Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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                                                                                   2123 bp DNA linear E amino acid sequence, Corynebacterium and process for producing L-amino aci
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                                                                                     ium microorganism acid.
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RS Tilke,I., Eggering,L., Eickmans,B., Zamu,H. and Meck,V.

Replicable DNA, amino acid sequence, Corynebacterium microorganism, shuttle vector, and process for producing L-amino acid Patent: JP 2001008693-A 1 16-JAN-2001;

DEGUSSA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH

OS Corynebacterium glutamicum
PN JP 2001008693-A/1

PD 16-JAN-2001

PD 16-JAN-2001

PP 24-MAY-2000 JP 2000153547

PF 24-MAY-2000 JP 2000153547

PF 27-MAY-1999 DE 19924365.4

PI IVENUE TILKE,LOTHAR EGGERING, BERNHARD EICKMANS, HERMANN ZAMU,
PI VETTYNA MECKEL
PC C12N15/09,C12N1/21,C12P13/04,C12P13/06,C12P13/06,C12P13/08, PC

C12P13/08,
PC C12P13/12,C12P13/20,C12P21/02//(C12N15/09,C12R1:15),(C12N1/21,
PC C12R1:15),
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PC C12R1:15),
PC C12R1:15),
(C12P13/04,C12R1:15),(C12P13/06,C12R1:15),(C12P13/08,C12R1:15), F
(C12P13/12,C12R1:15),(C12P13/20,C12R1:15),(C12P21/02,C12R1:15),
(C12P13/12,C12R1:15),(C12P13/20,C12R1:15),(C12P21/02,C12R1:15),
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                                                                                                        TCGATAGCCTAAATTGGGCTTAGATCTTCCGCCTCTAAATAGGTATGCAGAGACATTCGA
                                                                                                                                                                                                   ACGTCTAGGCAAAAAGTAGTTTTGTGAGATGAAACGCATAATCCGTCATTTTTTACGCAA
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_574 c 592 g 497 t
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	1621 GCTCCCCTCCCACCGTTTCGGTCATTATTGGTCAGGGCGTTGGCGGTGGCGCTGGCC 1680
gene	1561 GCGGCTGAGGAGCTCGGCATCGCAAGCTCGATTGCGCGCACCTTGTCCAAGCTTATCGAC 1620
	1501 CGCGAGCTAAACCTGCCGATCGTGTCCATCGACACCTCCGGGGCCCGAATTGTCGCAG 1560
FEATURES source	1441 CGCCGCTTCACGCTTGGGCCGCAGGAGCTGCGTTTTGCGCTGGCATTTCGCTGGCG 1500
JOUKNAL Submit Ltd., Tokyo Tel:81	1381 GCTGTGCGCGTTGGCGCGCATCGGGGGCCCGTGGTGCTGATTGGGCAGGAT 1440
REFERENCE 2 (based on the control of	1321 GAAACGTTGGGGGCAGACGTCGTCAAGCTTTCTGGTGCGGGTGCTGGCGGCATTGAGCCCCG 1380
	1261 GTGATGGAGGCGATTGCGCGTTCTCGTGACCCGCAGAGGCCTGGAATCGGGGAGATTATG 1320
KEYWORDS SOURCE Coryne ORGANISM Coryne Bacter	1201 ATTCAGCCGGTAGAGGCAACGGATCGTTTTTCTCCCAACAACTCCTGGCGTGGCACTTCCG 1260
ACCESSION AP0052 VERSION AP0052	1141 ATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAGCGGTGGCAAAAACCCTCAAGGTT 1200
	1081 ACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTGGTGAAAACTGGTGTG 1140
Oy 2101 GCCG	1021 ACTTTTGCGGAACCCGGCGCGCAGATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACC 1080
2041	961 TATTTGCGCAATCCCACGATGGGTGGCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTC 1020
1981	901 ATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTG 960
1921	841 CTGGTCTCCCCTGCTTCCGGTGGTGGTGGCGCATGCAGGAAGACAATCGAGCTTTTGTCATG 900
1861	781 GTCGCGTCGGTGCGCATCATGAAGGCGATTCACCGCGCCACAGAGCTGAAACTCCCACTG 840
1801	721 GGCATICCGGTAGCCGTTATTTTGTCCGAFTTTTCCTTCCTCGGCGGTTCTTTGGGCACG 780
1741	661 CGGGCTCGAAGCAAGGCCAAATGCGATGAATCGGTAATTACTGGAGAAGGCACCGTGGAG 720
1681	601 TCTTGGAATGAAACTCCCCAATATGACAACCTCAATCAAGGCTATGCAGAGACCTTGGAG 660
1621	541 ATGGAACACATTCAGCATTGACGCTCATAGACTCGGTTTTGGACCCTGACAGCTTCATT 600

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itted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.
Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,
5 194-6533, Japan (E-mail:snakagawa@xanagen.com,
91-44-829-3031, Fax:81-44-813-1651)
sequence is conducted by collaboration of Kyowa Hakko Kogy
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nebacterium glutamicum ATCC 13032
sria; Actinobacteria; Actinobacteridae; Actinomycetales;
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5276.1 GI:21323419
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nebacterium glutamicum ATCC 13032 DNA,
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VWLLLAPRDYLSTFMKIGVIGLLAVGILFAR PEVQMPSVYSKALEGIGPVFSGSLFFF
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                                                                                                                                                                                                                                                                                                                                                                                                  KEQDRFLDAAQRTHELEDLSELNIELDADILAKAPVIPEGLF"
                                                                                                                                                                                                                                                                                                                                                                                                                                VDPAEKAFGARAVITFKDGTVVEDELAVADAHPLGARPFAREQYIQKFRTLAEGVVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catabolism"
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complement (8265. .8987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENCSFEEVFYLLWHGELPTAQQLAEFNERGRSYRSLDAGLISLIHSLPKEAHPMDVMR
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                                                                                                                                                                                                                                                  complement (9094. .9798)
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                                                                                                                                                                                                                                                                                   KSILTALINADSTGSQGIDIRS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="PF00392:Bacterial regulatory proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="GI:21323427"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="PF02615:Malate/L-lactate dehydrogenase"
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3.1"
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661 13011 721	601 213071	541	Qy 481 AT	Qy 421 TC	Qy 361 AC	Qy 301 GT 	Oy 241 TC	Qy 181 AC	Oy 121 AP Db 213550 AP	Oy 61 CT Db 213610 CT	Oy 1 CT Db 213670 CT	Query Match Best Local Sim Matches 2122;				gene CDS	
	TCTTGGAATGAAACTCCCCAATATGACAACCTCAATCAAGCTATGCAGAGCCTTGGAG 660		540	480 21319	ACGTCTAGGCAAAAAGTAGTTTTGTGAGATGAAACGCATAATCCGTCATTTTTTACGCAA 420	GTGCAATAGTTAACGGGCTTCACACGTCACCATTCTGTCCGGGTTTTAGGCTATGTTCGGG 360	TCCCGATCTACCCCCTCTTACCCCGAAATACCCCCTTTTGCAAAGATTGCAAACACAACA 300	ACTCCCCCAATATCTTAACTTAAACTTAAAAGTAGTGTTTTACCTGCATTTATAAAAGT 240	AACGTGTGAAATGTGAAGTTACCTAACTCACATTGCAATGCGATAGCGATTTGGAAAACTC 180	CTTATATGTTTCTCACCACATCTGGCCGACGACCACGAAGTATGTTGTCGATCACAGCTA 120	CTCGAGCGGGAGTCGGTGATCGGCCACTCTCTAAGCAATGCCGGCTTTAAAATAAAGCAA, 60	99.4%; Score 2111; DB 1; Length 332050; Similarity 100.0%; Pred. No. 0; 2; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	/db_xref="G1:21323430" /translation="MAKIIWTRTDEAPILATYSLKPVVEAFAATAGIEVETRIJISLAG /translation="MAKIIWTRTDEAPILATYSLKPVVEAFAATAGIEVETRIJISLAG RILAGPFERLTBOQKVGWALAELGELAKTPEANIIKLPNISASVPQLKAAIKLLODGG YDIPELPDNATTDEEKDILARYNAVKGSAVNPVLREGNSDRRAPIAVKNFVKLFPHRM	/codon_start=1 /trans1_table=11 /product="Monomeric isocitrate dehydrogenase (NADP+)" /protein id="BAB98057.1"	ä	GIRAWINSKKOSKISO" COmplement(987812094) /gene="Cgl0664" Complement(987812094)	VVTFWNSIEDSVREQRLDELDAQDPGIKAAIESYIAQDDNAPTAAELQVRLDAIESGE GLAMLLPDDPTLADPNAEESFKTEYTYDEAKDIISGFSSDPASDVLSQLQQAATTGTR TAEIRAEVFADRTDDYNESQTALKEDFQNCIDAIDDARPIPLQYILIGGAIA\AVIVL
Qy bb Qy	B 8	₽ Q	B 8	pb dd	g 49	g dy	g 94 6	g da	א לא	B 64	망양	B &	DP OA	B &	D Qy	p &	Db
1741 GAGGGCGCCTCGGCCATCCTCTTCCGCGACACCAACCACGCCGCGGAAATCATAGAGCGA 1800	1681 ATGCTGCCCGCCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCA 1740	1621 GCTCCCCTCCCCACCGTTTCGGTCATTATTCGTCAGGGCGTTGGCGGTGGCGCTGGCC 1680	1561 GCGGCTGAGGAGCTCGGCATCGCAAGCTCGATTGCGCGCACCTTGTCCAAGCTTATCGAC 1620	1501 CGCGAGCTAAACCTGCCGATCGTGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCAG 1560	1441 CGCCGCTTCACGCTTGGGCCGCAGGAGCTGCGTTTTGCGCGTCGTGGCATTTCGCTGGCG 1500	1381 GCTGTGCGCGTTTGCCCTGGCGCGCATCGGGGGCCCGCCGGTGGTGGTGGTGGCAGGAT 1440	21 GAAACGTTGGGGGCAGACGTCGTCAAGCTTTCTGGTGCGCGTGCTGGCGCATTGAGCCCG	1261 GTGATGGAGGCGATTGCGCGTTGTCGTGACCCGCAGAGGCCTGGAATCGGGGAGATTATG 1320	01 ATTCAGCCGGTAGAGGCAACGGATCGTTTTCTCCAACAACTCCTGGCGTGGCACTTCCG		1081 ACTGGGCATGCGCTTCCACACGGTTGCACAGGCGGAGAATTTGGTGAAAACTGGTGTG 1140	1021 ACTTTTGCGGAACCCGGCGCACATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACC 1080	961 TATTTGCGCAATCCCACGATGGGTGGCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTC 1020	901 AIGGIGICCATAACCGCGGCTGIGCAGCGICACCGCGAGGCGCAITIGCCGIICCTGGIG 960 	841 CTGGTCTCCCCTGCTTCCGGTGGTGCGCGCATGCAGGAGAGACAATCGAGCTTTTGTCATG 900	781 GTCGCGTCGGTGCGCATCATGAAGGCGATTCACCGCCCCACAGGCTGAAACTCCCACTG 840	

, AO	Db Qy	Marches Qy	Query Best I	BASE COUNT	œ	TITLE JOURNAL FEATURES	REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM	LOCUS DEFINITION ACCESSION VERSION	RESULT 5	B 8	D Q	당	B 8	g 64	В
121 281500 181 281440 241 281380	81	nes 2122;	y Match Local	OUNT	rce	r				ภ เภ ว	2101	2041 211631	1981 211691	1921 211751	1861 211811	211871
AACGTGT AACGTGT AACTCCCC ACTCCCCC ACTCCCCAT ACTCCCGAT TCCCGAT	CTTATAT	CTCGAGC	p .	79274 a		ovel pol atent: E YOWA HAR	orynebac akagawa, okoi,H.	orynebac orynebac	AX127145 Sequence AX127145 AX127145.		GCCGACC	GTGGCCC	TAAAGAJ TAAAGAJ	AACAATO	ACCGAGO ACCGAGO	CAAGGC
GAATGTG	GTTTCTC	GGGAGTO	99.4%; larity 100.0%;	/mote=" 0.600.0	1349980 /organism= /mol_type=	ynucleo P 11087 CKO KOGY	terinea S., Miz Tateis	terium terium	7061 fr AX11412		TTCATGC	GAACCCT	VAATTATG VAATTATG	CCGGAGAG CCGGAGAG	CACTTTGT	FIGCAGGC
AAGTTACC AAGTTACC CTTAACTT CTTAACTT CTCTTTAC CTCTTTAC	ACCACATO	e U; GGTGATCC		Seq 1 tc 01 0.949 c 9872	980 sm="Cory	tides 90-A 706 O CO., I	e; Coryr oguchi, F hi.N., 8	Corynebacterium glutamicum Corynebacterium glutamicum Bacteria: Actinobacteria:	349 7061 from Patent AX114121 1 GI:14041133		GCCGACCTTCATGCCTGGAATTC	CAGGGCCC	CGCTGATO	GGCGGGA	TGAAGAAJ TGAAGAAJ	GCACGCA
TAACTCAC	TGGCCGA(M1 Smat	Score 2111; [Pred. No. 0;	/mcte="Edata": 1/10" / mote="Seg 1 to long (3.309. 0.600.001 0.949.980 '" a 90638 c 98727 g 81341 t	nebacte	1 20-JU TD. (JP)	Corynebacteriaceae; achi, H., Ando, S., Ha N., Senoh.A., Ikeda	um um	349980 bp D ent EP1108790. 3		C 2123	TAAGCAG	AAATCGA AAATCGA	GCGACAG 	ATTCTCGG	TTTTAAG
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                                            Pompejus,M., Kroeger,B., Schroeder,H., Zel
corynebacterium glutamicum genes encoding
membrane synthesis and membrane transport
Patent: WO 0100805-A 25 04-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
                                                                                                                                           Corynebacterium glutamicum
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                             GGAACCCGGCGCAGATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCA
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ARGALSPAVRVALARIGGFPVVLIGQDRFTTLGQPUSGIGEIMETLGADVVKLSG
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Tilg,Y., Eikmanns,B., Eggeling,L., Sahm,H. and Mockel,
Process for the preparation of L-amino acids by fermer
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Query Match 69.4%; Score 1473; DB 6; Length 1473; Best Local Similarity 100.0%; Pred. No. 0; Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Sob GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC 567	AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A. TITLE Novel polynucleotides JOURNAL Patent: EP 1108790-A 929 20-JUN-2001; KYOWA HAKKO KOGYO CO, LTD. (JP) FEATURES Location/Qualifiers SOURCE /organism="Corynebacterium glutamicum" /mol_type="genomic DNA" /mol_type="genomic DNA" /mb xref="taxon:1718" BASE COUNT 275 a 414 c 456 g 328 t	AX121013 N Sequence 929 AX121013 AX121013.1 Corynebacteri M Corynebacteri Bacteria; Act Corynebacteri	1381 GGCACAATCAGCAACGCCCTCTCCGAATTGGATAACAATCCGGAGAGGGCGGGACGCGAC 1 1948 AGTCGCTTCACACGATTTGAGCGTTTAGCGCAG 1980	QY 1.88 GACACHACCACCACCGCGAAATCATAGAGCGACAAGGCGACGGACG	1708 GCGAAAACGCGTGGCTGTCCGCATTGCCACAGGGGGCGCTCTGGCCATCCTCTCCGC 1	1021 ATCATCGACCCCTTCCCCCCCCCCCCCCCCCCCCCCCCC	Db 901 GGGGCCCGCTGGTGTCGCAATTGCGAAGCTGAAGAGCTGAAGATCGGAATCGGAACCTAAACCTGGGAATCGTGTCC. 1527 Qy 1468 CTGCGTTTTGCGCGTGGCATTTCGCTGGCGAGCTAAACCTGCGAATCGTGTCC. 1527
Oy 1528 ATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGCTCGGCATCGCAAGC 1587	Oy 1348 CTTTCTGGTGCGGTGGCGATCTGACCCGGCTGTGCGCGTTGCCGCTGGCGCGATC 1407	OY 1.16 TIGGIGGAGAGGCTIGGAAAACCCTCAAGGTTATTCAGCCGTAGAGGCAACGATCGT 1227	1048 GFTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTG	Qy 928 CGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGC 987	Qy 808 ATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGCTCCCCTGCTTCCGGTGGTGCG 867	Qy 688 GAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTTGTCC 747	Qy 568 ATAGACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGAC 627

1473; Conservative	Query Match 69.4%; Score 1473; DB 6; Length 1473; Best Local Similarity 100.0%; Pred. No. 0;	/mol type="genomic DNA" /mol type="genomic DNA" /mol type="genomic DNA" /db_xref="taxon:1718" BASE COUNT 275 a 414 c 456 g 328 t	CDS (1). CDS Location/Qualifie 1. 1473	/00, 2N15/00,C12R1:15) Incation/Oualifiars	PC C12R1:15), PC C12R1:15), (C12P13/04, C12R1:15), (C12P13/06, C12R1:15), (C12P13/08, C12R1:15), PC (C12P13/12, C12R1:15), (C12P13/20, C12R1:15), (C12P21/02, C12R1:15), PC	12P13	PD 16-JAN-2001 F000153547 PD 24-MAY-2000 JP 200153547 PR 27-MAY-1909 IP 19924355.4 PI TVENUE TILKE LOTHAR EGGERING BERNHARD EICKMANS. HERMANN ZAMU.	JOURNAL PATENT: JP 2001098693-A 2 16-JAN-2001; DEGUSSA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMBH COMMENT OS COTYNEDSCETTUM GIUTAMICUM DISTRIBUTION OF COTYNEDSCETTUM GIUTAMICUM	REFERENCE 1 (bases 1 to 1473) AUTHORS Tilke,I., Eggering,L., Eickmans,B., Zamu,H. and Meck,V. TITLE Replicable DNA, amino acid sequence, Corynebacterium microorganism, shuftle vector and process for producing L-amino acid shuftle vector.	SM Cor Bac	shuttle vector, and process for pro BD004742 BD004742.1 GI:18632703	RESULT 9 BD004742 BD004742 BD004742 BD004742 DVA linear PAT 31-JAN-2002 DEFINITION Replicable DNA amino acid seguence. Corynabacterium microorganism.	Db 1441 AGTCGCTTCACACGATTTGAGCGTTTAGCGCAG 1473	1381 GGCACAATCAGCACCCCTCTCCGAATTGGATAACAATCCGGAGAGGGCGGGACGCGAC	1828 1321 1886	170 GACACCACCCCCGAAATCATAGAGCGACAAGGCGTGCAGGCACGCAC	170 GCCGAAAACGCGTGCCGCATTGCCCACAAAGGGCGCCTCGGCCATCCTTCCGC 1201 GCCGAAAACGCGTGGCTGTCCGCATTGCCACAAAGGGCGCCTCGGCCATCCTTCCGC	1141
1588	QY 1528 ATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGCTGAGGAGCTCGGCATCGCAAGC	Qy 1468 CTGCGTTTTIGCGCGTCGTGGCATTTCGCTGGCGCGAGCTAAACCTGCCGATCGTGTCC	Qy 1408 GGGGCCGGCCCGTGGTGCTGATTGGGCAGGATCGCCGCTTCACGCTTGGGCCGCAGGAG	Qy 1348 CTTTCTGGTGCGCGTGCTGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCCTGGCGCGCATC	QY 1288 GACCCGCAGAGGCCTGGAATCGGGGGGAATTATGGAAACGTTGGGGGGCAGACGTCGTCAAG	1228 721	Qy 1168 TTGCGTGCAGCGGTGGCAAAAACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGT	Qy 1108 CAGCAGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATT	Qy 1048 GGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTG	Qy 988 GCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATA	Qy 928 CGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGTGGC	Qy 868 CGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAG	9y 808 ATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCGGTGGTGCG	Qy 748 GATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCG	Qy 688 GAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCC	Qy 628 AACCTCAATCAAGGCTATGCAGAGACCTTGGAGGGCTCGAAGCAAGGCCAAATGCGAT	Qy 568 ATAGACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGAC	Qy 508 GTGGAGAAGCGTTTTCCGACTATGGTGGGGGCATGGAACACACTTCAGCATTGACGCTC
	CAGGCGGCTGAGGAGCTCGGCAAGC 1587	GCGCGCGAGCTAAACCTGCCGATCGTGTCC 1527	ATCGCCGCTTCACGCTTGGGCCGCAGGAG 1467	CCGCTGTGCGCGTTGCCCTGGCGCGCATC 1407	TIGGAAAGTITGGGGGCAGAGGICGICAAG 134/ 		TTATTCAGCCGGTAGAGGCAACGGATCGT 1227 	JTGATTGATGGAATTGTGTCGCCACTCCAA 1167	ACCACTGGGCATGCGCTTCCAGACGGTGTG 1107	TCACTITTGCGGAACCCGGCGCAGATA 1047 	TGTATTTGCGCAATCCCACGATGGGTGGC 987	ATGATGGTGTCCATAACCGCGGCTGTGCAG 927	TGCTGGTCTCCCCTGCTTCCGGTGGTGCG 867	ACGGTCGCGTCGGTGCGCATCATGAAGGCG 807	AGGGCATTCCGGTAGCCGTTATTTTGTCC 747 	AGCGGGCTCGAAGCAAGGCCAAATGCGAT 687	ATTICITGGAATGAAACTCCCCAATATGAC 627	GCATGGAACACACTTCAGCATTGACGCTC 567

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PN JP 200:
PD 09-JUL-
PF 15-DEC-
PI SAROSH!
PI HARUHIK
PI OZAKI
PC C12N15/
PC C12N15/
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Nakagawa, S., Mizoguchi, H., Ando, S.,
Yokoi, H., Tateishi, N., Senoo, A., Ik
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C12P19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC
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11: JP 2002191370-A 929 09-JUL-2002;
A HAKKO KOGYO CO LTD
Corynebacterium glutamicum
JP 2002191370-A/929
09-JUL-2002
19-DEC-2000 JP 2000405096
SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
KEIKO OCHIAI,
HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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    Hayashi, M., Ochiai
    Ikeda, M. and Ozaki, A.

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                                                                                                                 GGGGCCCGCCCGTGGTGCTGATTGGGCAGGATCGCCGCTTCACGCCTTGGGCCGCAGGAG 1467
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                                                                                                                                                                                CTTTCTGGTGCGCGTGCTGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCCTGGCGCGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                               TTGCGTGCAGCGGTGGCAAAAACCCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGT
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•	FEATURES	TITLE COMMENT F			194 144 T 11 217/c			Db 1021 Qy 1588 Db 1081 Qy 1648 Db 1141
	Ibaraki, 305-8566 Japan Nakamura, Y., Ikeo, K., Suzui National Institute of Genetic Itoh, T. is at the Japan Bio Koto-ku, Tokyo, 135-0064 Japan Yamagishi, A. is at Tokyo Un Hachioji, Tokyo, 192-0392 Jaj Nishio, Y., Usuda, Y. and Su, Inc., Kawasaki, Kanagawa, 21 The other authors are at the Evaluation, Shibuya-ku, Toky Loccation/Qualifiers	Direct Submission. Submitted (17-MAY-: National Institute Center; Nishihara ([E-mail:bio@nite.go Kawarabayasi, Y is Institute of Advan	Xawarabayasi,Y., Yamazaki,J., Hin Ikeo,K., Suzuki,M., Mashima,J., I Usuda,Y. and Sugimoto,S. The entire genomic sequence of Co Published Only in Database (2002) 2 (bases 1 to 300750) Kawarabayasi,Y., Yamazaki,J., Hin Director-General of Biotechnology	AP00521/ Corynebacterium efficie 4/11. BA000035 AP005217.1 GI:23492722 Corynebacterium efficie Corynebacterium efficie Bacteria; Actinobacteri Corynebacterineae; Cory	AGTCGCTTCACCACGAT	AGCCAAGGGCTTATCG AGCCAAGGGCTTATCGI GGCACAATCAGCAACGG [GCCGAAAACGCGTGGC:	TCGATTGCGCGCACCTTCGATTGCGCGCACCTTTCGATTGCGCGCACCTTTCGATTGCGCGCACCTTTGCGTCAGGGCGTTGCATTGGTCAGGGGCGTTGCAGGGGCGTTGCAGGCGTTGCAGGGCGTTGCAGGGCGTTGCAGGGCGTTGCAGGGCGTTGCAGGGCGTTGCAGGGCGTTGCAGGGCGTTGCAGGGCGTTGCAGGGCGTTGCAGGGCGTTGCAGGCGTTGCAGGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGAGGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGCGTTGCAGGCGCGCGTTGCAGGCGCGTTGCAGGCGCGTTGCAGGCGCGTGCAGG
	Ibaraki, 30-8566 Japan Nakamura, Y., Ikeo, K., Suzuki, M. and Mashima, J. are at the Nakamura, Y., Ikeo, K., Suzuki, M. and Mashima, 411-8540 Japan National Institute of Genetics, Mishima, Shizuoka, 411-8540 Japan Itoh, T. is at the Japan Biological Information Research Center, Koto-ku, Tokyo, 135-0064 Japan Yamagishi, A. is at Tokyo University of Pharmacy and Life Science Hachioji, Tokyo, 192-0392 Japan Nishio, Y., Usuda, Y. and Sugimoto, S. are at the Ajinomoto Co., Inc., Kawasaki, Kanagawa, 210-8681 Japan The other authors are at the National Institute of Technology and Evaluation, Shibuya-ku, Tokyo, 151-0066 Japan. Location/Qualifiers	Direct Submission Submitted (17-MAY-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, Tel:81-3-3481-1933, Fax:81-3-3481-8424) Kawarabayasi, Y is officially affiliated with the National Kawarabayasi, Y is officially affiliated with the National Institute of Advanced Industrial Science and Technology, Tsukuba,	Kawarabayasi,Y., Yamazaki,J., Hino,Y., Kikuchi,H., Naka Ikeo,K., Suzuki,M., Mashima,J., Itoh,T., Yamagishi,A., Usuda,Y. and Sugimoto,S. The entire genomic sequence of Corynebacterium efficier Published Only in Database (2002) (bases 1 to 300750) Xawarabayasi,Y., Yamazaki,J., Hino,Y., Kikuchi,H. and Director-General of Biotechnology Center.	ns YS-314 DN ns YS-314 DN ns YS-314 ns YS-314 ns YS-314 ns YS-314 ns YS-314	AGTCGCTTCACACGATTTGAGCCAG 1980	AGCCANGGGCTTATCGACGGGATCGTCGCGATACCGAGGACGGGGGGGG	GCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCTCGGCCATCCTTTCCGC	ATTGGTCAGGGGGTTGGCGGTGGCGGTCAGCGTGAGGAGCTCGGATCTACGGGGTAGAGCTTGGTCAAGCTATCGATCG
	nd Mashima, J. are ima, Shizuoka, 411 Information Resear of Pharmacy and L S. are at the Ajin apan 1 Institute of Tec. 066 Japan.	eral of Biotechnol. Evaluation, Biote u, Tokyo 151-0066, 1-1933, Fax:81-3-3- ated with the National ence and Technolog	т р	A, complete genome, i teridae; Actinomyceta	173		AGGGGGCTTCGGCCATCCTAGGCGAGCGAGGGAGGGAGGG	GGCTGAGGAGCTCGGCA
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Complement (12229. .12822)

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identity: 71 in 195 aa"
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LLEEARWIGAVAGGGVTSPARVLTQAPAGVIPEIADIAVAVRAPKFVDYFIVQADYTV
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MVPGFLQPEMQKIIGQLADLESPGLASVYRISEASLRHAMDLGLTATEIEDFLTQAPTVA
TGLPQSVAYLLQDIARRHGTLRGGPALCYLRSDDPALHSAVEAGALGLRQIAPTVA
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GQVDALDESTGAVHRFMLHRITEVIVD"
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GREGDVFSLIGFRGDAFWCDLEAQGFTATADCVBVFTTWTDAERMYYATAETADRYE
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COMplement (9548 . 11851)
/note="CE0892, similar to AE006976-11|AAK45126.1| percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="mpcfpfsqirqtkytstapklgdimkkdspyptltgwleqlddd
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TNWQLLPEEHGRSLTFGEASQSIEALPARHRKILVTLYTSNGLGLTRDAALSADPARP
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/note="CE0891, similar to AL583924-93|CAC31112.1| percent
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/db/xref="GI:3842778"
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DEISPWPITWGTDADVVRRAEKTIPHDLWNKLEKNRNRLDEVKNTRNMLLVL"
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ASLPGMWDRT I TVSSAAKTENVTGWKTGWALABAPI LEBAVI TAKQPMS YVGATPFQPA
VAHAVAHEKPWYKQMKKGLQNKRD I LTDALTQAGLKVHDSHGTYFVVADIGERGGAEF
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                                                                                                                                                                                                    xref="GI:23492731"
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Query Match
Best Local Similarity
Matches 1046; Conserv
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                                                                                                                                                                                                            GAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAGCGGTGGCAAA 1187
                                                 CGTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTGACCCCGCAGAGGCCTGGAAT 1307
                                                                                                        GATCATGAGGGTGTTGGGGGAGGCGTCGCCAGGCACGCCCGTGAGCTCGCCGCACCCGG
                                                                                                                                                       AACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTTCTCCCAACAACTCCTGG 1247
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/protein id="BAC17705.1"
/db_xref="GI:23492733"
/translation="wpv92773WYDPERGFGFVSNPGGEDCFVGKQVLPKGVTELHQGQ
RIEFDFAAGRKGPQALRVKVLETPRRRPQHTYKPEELNGIISDMVTMLEGTVQPALLK
GHYPDRKVGEQVAKILRAVAKELEA"
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DRLANCESGGNWAINTGNGYHGGLQFSPSTWRAYGGDEFAPFAYQATREQQIAVAERT
LAGQGWGAWPACSSKLGLNSAPTPRNLNPAPAPAPAPAAPAEYRATVDTNTNPVVGSS
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citrate synthase; glt gene.
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 Sahm, H.
Nucleotide sequence,
Corynebacterium glut
                                                                                                                                           C.glutamicum glt
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                                      Eggeling, L.,
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Direct Submission
Submitted (15-MAY-1992) B.
Forschungszentrum Juelich
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TCCGAATTGGATAACAATCCGGAGAGGGCGGGACGCGACAGTCGCTTCACACGATTTGAG
                                                                                            ATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTCGGCACAATCAGCAACGCCCTC
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                                                                   ATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTCGGCACAATCAGCAACGCCCTC
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838. .2151
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FETGEEFDSSWDRGQTSQFPLNGLIAGWQEGIPGMKVGGRRQLTIPPEAAYGPEGSGH
PLSGRTLVFIIDLISA"
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etglitedegyvstgsteskityidodagilryrgvdiadlæratenevsyllinge
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ldeagldkatvrlmakvpmlaayahrarkgapymydnnslanænflænflyptepy
Eldpimvkaldkiliihadheqncststvrmigsaganmfvsiagginalsgflhgga
nqavlemlediksnhggdatefmnkvknkedgvrlmgfghrvyknydpraaivketah
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FAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGNESRKLVPREER"
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/db_xref="SWISS-PROT:P42458"
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/protein_id="CAA46902.1"
/db_xref="GI:505581"
/db_xref="SWISS-PROT:P42457"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, C. Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
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Mycobacterium tuberculosis CDC1551
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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AE006979 AE000516
AE006979.1 GI:138
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Unpublished
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                                                                                                                                                  / trānslation="MosratyObfsdsypechingerpimmekiivsyOhstrrhiitsev
GrkarlindvrrllsdkrlvtlitgedgmgksrlalqigaqiahetyTgrwdcdlatytd
RDCVSISMLNALGLPVQPGLSAIDTLYGVINDARVLLVLDHCBHLDACAAIIDSLTR
SCERLTILTTSTEAIGLAGELTWRVPPLSLTNDAIELFVDRARRVRSDFAINADTAVT
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                                                                                                  VGBİCRRLDGVPLAIELAAARTDTLSPVEILAGLNDRFRLVAGAAGNAVRPEQTLCAT
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                                                                                                                                                                                                                                                                                                                                                                                          note="identified
                                                                                                                                                                                                                                                                                                                                                                                                               gene="MT0918"
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CFLYHLAGATAWALDPDGTVRYHS
CFLYHLAGATAWALDPDGTVRYHS
DGSDGAEHLVRGRFYLLVGVYTBAVLASLIGEFVAALAPGAQVKVIMVVRRLPRILDDGY
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LLIGFTGEPRAAHLAAIGAAPDAHGFAAFYRRCRLVTARLWTTLIEPLRTREQARRDI
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VAKHTAPPRGSSRPLTLAKGVLGQARGVPGMVRVVADTTWRAAQCRSGPLTLAAPHTPL
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                                                                     /translation="mGKGRKPTDSBTLAHIRDLVAEEKALRAQLRHGGISESEEQQQL
RRIEIELDQCWDLLRQRRALRQTGGDPREAVVRPADQVEGYTG"
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MLEGIRDSGDDVSEFVRKVKNREAGVKLMGFGHRVYKNYDPRARIVKEQADKILAKLG
GDDSLLGIAKELEEAALTDDYFIERKLYPNVDFYTGLIYRALGFPTRMFTVLFALGRL
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fdvgfantaaakssityidgdagilryrgyfdiqlakstfievcylliyggledtdq
laottgtichtlaktletikefbgfpranhypvlssvvalsayyodalelyrungov
Elstirliakletiaayaykksvgofflyfdnsltivenflrltfgffaefyoadpev
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/codom creen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGWIAHWREMHDEGDSKIGRPRQIYTGYTERDYVTIDAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trans1_table=11
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3093. .4388
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                                                                                                                                                                                                     transl
                                                                                                                                                                                                                                                                               gene="MT0921.
                                                                                                                                                                                                                                                                                                                                  'gene="MT0921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MT0921"
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                                                                                                                                             al protein"
9.1"
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                       SRAGVETATDDNGSGVPEGERQVVFERFSRGSTASHSGSGLGLALVAQQAQLHGGTAS
LENSPLGGARLVLRLPGPS"
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                                                     translation="MGGMDTGVTSPRVLVVDDDSDVLASLERGLRLSGFEVATAVDGA/
                                                                                                                                                                                                                                                                                                                 complement (9473. .10183)
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7575. .8105
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7426. .7578
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     14.7%;
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  Score 312.6;
  DB 1;
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1574 TCGGCATCGCAAGCTCGATTGCGCGCACCTTGTCCAAGCTTATCGACGCTCCCCTCCCCA 16	13	1514 TGCCGATCGTCGATCATCGACACCTCCGGCGCCCGAATTGTCGCAGGCGGCTGAGGAGC 15	1454 TTGGGCCGCAGGAGCTGCGTTTTGCGCGGTCGTGGCATTTCGCTGGCGCGCGAGCTAAACC 15		9 GGGGCCGGCCCGTGGTGCTGATTGGGCAGGATCGCCGCTTCACGC 1	1349 TTTCTGGTGCGCGTGCTGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCCTGGCGCGCATCG 14	11050 GGCCGGACCGGCGTCAGGCAGCTACTGCGACACGGCGCCACCGACCG	1289 ACCCGCAGAGGCCTGGAATCGGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAGC 13	ATGTGCCCACGTGGGACTCGGTGGTGGCATCGCGCC 1		GACCGATGCTGGATCGTGGGTTGACGGTGCTCATCGACGCTCCCGAACCGCTTCCGGCAC 1	1172 GTGCAGCGGTGGCAAAAACCCTTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTT 12	0 CCGCCGAGAATCTACGGCGCATGGGATCATCGACGGCGTCGTTGCACTGGACCGGCTAC 1	ш	290 TTCTGGGACCACGGGTCTATGAGTTGCTCTATGGCGACCCCTTCCCATCCGGCGTCCAAA 1	1052 TCCTGGGTCCTCGCGTGGTGGTAGTTAACCACTGGGTATGCGCTTCCAAACGGTGTGTGCAGC 1	992 TIGGCCTICGTIGGGTTCATCTGGGCATCTCACTTTTGCGCAACCCGGCGCGCAATAGGTT 1	10 ACAACCAGGCGCGCCTGCCCTACCTGGTCTATTTGCGCCATCCGACCACGGGTGGAGTTT 1	932 ACCGCGAGGCGTTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCA 9	11470 TGCAAGAAGGCACGGTCGCGTTTCTGCAGATGGTGAAGATCGCTGCGGCCATCCAGCTGC 1	9	11530 AGCGGGCGAGCGGCGGCTGCCGCTACTGGCGTCACCAAGCTCGGGAAGCACCCGCA 1	70 I CHARLIICLIGADA GALLAGA I LAGAGI GALLAGA G	752 TITCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGGATCATGAAGGCGATTC E	50 CGGTGCAGACCGGTGAGGGACGCGTATTCGGGCGGGGGGGG	7		632 TCAATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGCCAAGGCCAAATGCGATGAAT 6		U U	Local Similarity 54.0%; Pred. No. 3e-60; Endels 21; Gaps:
ω ω	754	73	.513	œ	453	.408 .0934)991	48	.051	88	1111	31	1171	171	1231	111	.051	135	91	141	31	147	153	, ,	159	51	1165	91	1171	31	ω

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
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available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projecte/M tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
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On Jur
Notes:
                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis H37Rv
Mycobacterium tuberculosis H37Rv
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium, Mycobacterium
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Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.
273101 AL123456
                                                                                                                                                                                                                                                                                                                            Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill,J
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1 (bases 1 to 37630)
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                                                                                                                                                                                                                                                                                                                                                                                      Jun 27, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 37630)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:3261565
                                                                                                                                                                                                                                                                                                                                                                                    replaced gi:1314009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCT 03-AUG-2001
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Rv0876c, '(MTCY31.04c), len: 548; unknown; possible membrane protein, highly similar to MLCB57 12 Mycobacteriumleprae cosmid B57 033057 HYPOTHETICAL 61.7 KI PROTEIN (790an) TOTAL CONTROLLED (190an) TOTAL CONTROLLED
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/trans1_table=11
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ANTTSTLFRPDTRLAVTIPTVDPQRGRLTGIVVQLLTLVVDHSGELRDVPHAEWSVRL
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RPPLQRLREIVEGLSPDERALVSHGLQIGIVVDEHLAAPGQGDFVIRGLLGADPSTGS
IRIDEVQUGATMGFQVRDAAGADKOLRLTTERAAARLPGRAAGALLFTCNGRGRRMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Rv0876c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN (579aa). FASTA scores: E(): 0; 81.0% identity in 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Rv0876c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Rv0875c, (MTCV31.03c), len: 162, unknown, possibly exported protein, highly similar toMLCB57_II Mycobacterium leprae cosmid B57, 033056 HYPOTHETICAL 18.1 KD PROTEIN (162aa). FASTA scores: opt: 789 z-score: 963.4 E(): 0;
                                                                                                                                                                                                                                                                                                                                     /product="hypothetical
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/db_xref="GI:1314013"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Rv0875c"
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/transl_table=
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aa overlap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Rv0878c, (MTCY31.06c), len: 443, unknown; similar to YHS6 MYCTU P42511 hypothetical 50.6 kd protein in hsp65 3' region, (517 aa), FASTA scores: opt: 1044, z-score: 954.9, E(): 0, (47.4% identity in 397 aa overlap). Similar also to MTV014_3; MTC165_2, MTCY98_24, MTCY3C7_23, MTCY3E_17, MTV004_5, MTV004_3 etc."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Rv0877"
/note="Rv0877, (MTCY31.05), len: 262, unknown,
/note="Rv0877, (MTCY31.05), len: 262, unknown,
equivalentto MLCB57_13 Mycobacterium leprae cosmid B57
equivalentto MLCB57_13 Mycobacterium leprae cosmid B57
033058 HYDOTHETICAL 28.2 KD PROTEIN (269 aa; E(): 0;80.5%
identity in 257aa overlap.)"
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NFAGNETSARLQLGRPAVLVVRCTVLLVTLAIAAAVAGSLAATALTITAGSSALAK
ASLDASLQHDLPEESRASGFGRSESTLQLAWVLGGAVGVLYYTELWVGFTAVSALLIL
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6442. .6873
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complement (5989. .6264)
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complement(5989. .6264)
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complement(4380.
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3583. .4371
                                                                                                                                                                                        overtap
                                                                                                                                                                                           /gene="Rv0879c"
/gene="Rv0879c, (MTCY31.07c), len: 91 unknown, equivalent
/note="Rv0879c, (MTCY31.07c), len: 91 unknown, equivalent
to MLCB57 14 Mycobacterium leprae O33059 HYPOTHETICAL 9.8
KD PROTEIN (91 aa), E(): 1.2e-25, 76.9% identity in 91 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA97385.1"
/db_xref="GI:1314016"
/db_xref="SWISS-PROT:Q10540"
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3583. .4371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="PPE"
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                                        6873
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/note="Rv0880, (MTCY31.08), len: 143, unknown, equivalent to MLCB57 15 Mycobacterium leprae cosmid B57 (143 aa) 033060 HYPOTHETICAL 15.8 KD PROTEIN. FASTA scores: opt: 818 z-score: 980.3 E(): 0; 89.5% identity in 143 aa overlap."
/codon_start=1
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Similarity TTGGGCCGCAGGAGCTTTTGCGCGTGGCATTTCGCTGGCGCGCGAGCTAAACC ACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAGC 1348 CCGCCGAGAATCTACGGCGGCATGGGATCATCGACGGCGTCGTTGCACTGGACCGGCTAC GGCCGGACCGGCCGGGCGTCAGGCAGCTACTGCGACACGGCCGACCCGACCGGGTGTTGT GTGCAGCGGTGGCAAAAACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTT 1231 TCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGC TGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCGCAGATAGGTT TCAATCAAGGCTATGCAGAGACCTTGGAGGGGGTTCGAAGCAAGGCCAAATGCGATGAAT ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG 35598 GGGCCGGCCCGTGGTGCTGATTGGGCAG----TTTCTGGTGCGCGTGCTGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCTGGCGCGCATCG CGCAGACGCCCGCCCCGTACCCGATGTGCCCCACGTGGGACTCGGTGGTGGCATCGCGCC CTCCAACAACTCCTGGCGTGGCA---CTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTG 1288 GACCGATGCTGGATCGTGCGTTGACGGTGCTCATCGACGCTCCCGAACCGCTTCCGGCAC AGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAATTGC TTCTGGGACCACGGGTCTATGAGTTGCTCTATGGCGACCCCTTCCCATCCGGCGTCCAAA TCGCGTCGTGGGGCTCGCTGGGGGCATCTCACCGTCGCCGAGCCGGGCGCCCTGATCGGCT ACAACCAGGCGCGCCTGCCCTACCTGGTCTATTTGCGCCCATCCGACCACGGGTGGAGTTT TGCAAGAAGGCACGGTCGCGTTTCTGCAGATGGTGAAGATCGCTGCGGCCATCCAGCTGC TGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTC AGCGGGCGACCGCCGAGCGGCTGCCGCTACTGGCGTCACCAAGCTCGGGAGGCACCCGCA ACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCGCGCA TTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTC 811 CGGTGCAGACCGGTGAGGGACGCGTATTCGGGCGGCGGGTGGCCGTGGTGAGT CGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATT ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC TGTCAGGAACCGATCAAGGCGAAGCG----GCGACCACGCTGCTGGCGCTGGCCCGCTTTG ACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCA TCGACTTCCTGGGCGGCTCGATTGGGGTGGCAGCGGCCGAACGGATCACCGCCGCCGTCG 14.7%; 54.0%; ĠĠŦĊĊŦĊĠĠĊĊĂĠĊAĄĄĠĠĠĊĄĠŦĄĠĠĊĠĠĊĠĠĠĠĠĄĄĠĊĂĊŦĠ 0; Score 312.6; DB Pred. No. 3e-60; Mismatches 589; GATCGCCGCTTCACGC 37630; 35178 1513 34761 1408 1171 1111 1453 34878 34938 34998 35058 35118 1051 35238 991 35298 931 871 751 691 631 34821 35358 35418 35478 35538 w

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                                                                                                                                                         Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex 15, France. e-mail:tegarnier@pasteur.fr Submitted on behalf of the Mycobacterium bovis sequencing teams, TB Research Group, Veterinary Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlestone, Surrey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK. PT4 Annotation, Genopole, Institut Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France. Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Online Publication PNAS 10.1073/pnas.1130426100 ( Microbiology ) 2 (bases 1 to 327650)
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium, Mycobacterium
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                                           /mol_type="genomic DNA"
/strain="AF2122/97"
                                                                                         organism="Mycobacterium bovis subsp. bovis AF2122/97"
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(99.9% identity in 882 aa overlap). Probable transcriptional regulatory protein, LuxR family, highly similar (but shorter 238 aa in N-terminus) to NP 302202.1 NC 002677 possible transcriptional regulator from Mycobacterium leprae (1106 aa). Also highly similar (generally in part) to others e.g. T50568 probable multi-domain regulatory protein from Streptomyces coelicolor (1334 aa); P10957 NARL ECOLI nitrate/nitrite response regulator protein from Escherichia coli (216 aa), PASTA scores: opt: 193, E(): 6e-06, (37.4% identity in 99 aa overlap); etc. Also highly similar to others from Mycobacterium tuberculosis e.g. MTCY02B10_22, MTV008_44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="mb09132, citA, len: 373 aa. Equivalent to Rv0889c, len: 373 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 373 aa overlap). Probable citA (alternate gene name: gltA), citrate synthase 2 (EC 4.13.7), highly similar to others e.g. CAB95999. I|AL35998 putative citrate synthase from Streptomyces coelicolor (387 aa), F39119|CISY_BACSU citrate synthase II from Bacillus subtilis (366 aa), FASTA scores: opt: 586, E(): 5.8e-30, (33.8% identity in 367 aa overlap); etc. Also similar to Rv0896|MTCY31.24 from Mycobacterium tuberculosis (29.2% identity in 274 aa overlap) and Rv1131. Contains PS00480 Citrate synthase signature. BELONGS TO THE CITRATE SYNTHASE FAMILY."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="Mb0914c"
complement(3413. .6061)
complement(3413. .6061)
/locus_tag="Mb0914c"
/note="Mb0914c, -, len: 882 aa. Equivalent to Rv0890c,
len: 882 aa, from Mycobacterium tuberculosis strain H37Rv,
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/protein_id="CAD93774.1"
/db_xxef="GI:31617665"
/txans1ation="WITVPENETVEGLDGVVAFTTEIABPDKDGGALRYRGVDIEDLVS
QRVTFGDVWALLVDGNFGSGLPPAEPFFLPIHSGDVRVDVQAGLAMLAFIWGYAFLLD
IDDATARQQLARASVWALSYVAQSARGIYQFAVPQRIIDECSTVTARFWTRWQGEPDP
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KKSKMPSQTPFEPFILMPIGVPFSDGLMTLSEFKVQELDRQTMYECTSDNCLTILKGF
TYSQMRLPGGDTVDVYUHLTMYTGGFPTMANLAQVANVIQONSAGRAVITYGDFBARS
SDDQSALLQFAQVNGLTDAMVQVEHGPTTPPFAPTCMVGNECELLDKIFYRSGQGVTL
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ENRTFVANPQQVSVPEGGTVGPVRFDACDPDGNRMTFAVRERGAPGGPQHGI VTVDQR
TASFI YTADPGFVGTDTFSVNVSDDTSLHVHGLAGYLGPFHGHDDVATVTVFVGNTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPMLDEVERAGDARSVVKGILDRGEKLMGFGHRVYRAEDPRARVLRAAAERLGAPRYE
VAVAVEQAALSELRERRPDRAIETNVEFWAAVVLDFARVPANMMPAMFTCGRTAGWCA
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complement (2205. .3326)
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complement (2205. .3326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contains possible N-terminal signal sequence."
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transl_table=11
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/protein_id="CAD93773.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="Mb0912"
/note="Mb0912, -, len: 490 aa. Equivalent to Rv0888, len:
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698. .2170
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EC_number="2.3.3.1"
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/transl_table=11
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/note="Mb0915C, ", len: 285 aa. Equivalent to Rv0891C, len: 285 aa, from Mycobacterium tuberculosis strain H37Rv, (99.6% identity in 285 aa overlap). Possible transcriptional regulator, highly similar in N-terminus to NP_302202.1 |NC_002677 possible transcriptional regulator from Mycobacterium leprae (1106 aa). Also highly similar to several Mycobacterium tuberculosis putative transcriptional regulators e.g. Q1102 |MTCY02B10 22 PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN (1159 aa), FASTA Scores: opt: 702, E(): 8.3e-40, (50.6% identity in 247 aa overlap); MTV036 21; MTV008 44; MTCY02B10 23 shows similarity with several adenylate cyclases and hydrolases from other organisms."
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ELLGACPELTI LATSREFI GMACELTREVESMSI TDEAVELFADRESKYOPGFT LANY
NAAAVGEI CRRLDGI PLAI EFAAARVRAMS PLE I ADGLDDCFRLLAGGVRGAVQRQQT
LRAS I I MSHALLITET RQIL EFAAARVRAMS PLE I ADGLDDCFRLLAGGVRGAVQRQQT
LRAS I I MSHALLITET RQIL EFAAARVRAMS PLUE JANGSDLDP SVLDQJTLLVD
KSLVVADDCQGRTRYRLLET VRRYALEKLGDSGEADVRAHRDYYTALASLNIPPADN
DHQRLVARAETEEI DUNLRAA FAMSREMGHI TI TEALQLAS SLQP I WFGRAHLREGLSWFNS
I LEDQRFHRLAG STAVRARALADKAMLSTWLATSSVGATDI I APAQQALAMAREVGDP
AALVRALTACGCSSGYNABEAAAPYFAERTDLARA I DDKWTLCQI LYWRCVGTCI SGDP
NALRAAAEECRDLADTIGDRF VSRHCSLWLSIAQMWAGNLTEALELSRE I TAEAEASN
DVPTKVLGLYTQAQVLAYCGASSAHAI JAGCI AAATELGGVYQGI GYAAMTYAALAAG
DVTAALEASDAARFILRAQOTBQVTRYI WDAGYQASVTALRAGGDAL AARQFANDAVDATMGWH
RWAALTIRARVATARGEPELARDDAHAALAGGAELHI YQGMPDAMELLAGLAGEAGEVGSH
SEGVRLLGAAAALRQOTRQVRFXI WDAGYQASVTALREAMGDDEDFARMAEGAALSTD
EALAYAQRGRGERKRARARGGSLTFTEEDVVRLVSEGLSNKDI AKRLFVSPRTVQTHL
TUTVA TOTA DEGUTY TUTPAN DOCCAG.
             CAB59668.1|AL132674 monooxygenase from Streptomyces coelicolor (519 aa), P12015|CYMO_ACIS cyclohexanone monooxygenase from Acinetobacter sp. (542 aa), FASTA scores: opt: 489, E(): 6.8e-26, (30.3% identity in 492 aa overlap); etc. Also highly similar to Rv0565c, Rv3854c,
                                                                                                                                                                                                                              /note="Mb0916, , len: 495 aa. Equivalent to Rv0892, 1 495 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 495 aa overlap). Probable monooxygenase (EC 1.14---), highly similar to others NP_250787.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAD93776.1"

/db_xref="GI:31617667"
/translation="MLFNAVHNSLPPNIDIDHAILRGEDHPPTCAKCVARGRISALGS
/translation="MLFNAVHNSLPPNIDIDHAILRGEDHPPTCTVTLLLADVEEST
LDLRYHSLRCYAAPPDVGRCEFVPPRRRVLIANQGLDVSRLPPTGTVTLLLADVEEST
HLWQMCPEDMATAIAHLDHTVSBAITNHGGVQPVKRYEGDSFVAAFTRASDAAACALD
LQRTSLAPIRLRIGLHTGEVQLRDELYVGPTINRTARLRDLAHGGQVVLSAATGDLVT
GRLPADAWLVDLGRHPLRGLFRPEWVMQLCHPDIREKFPPLRTAKSSFTSILFAQFTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVGRRAQIS"
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/transl_table=11
/product="possible_transcriptional_regulatory_protein"
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/protein_id="CAD93775.1"
/db_xref="GI:31617666"
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etc
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Best Local Similarity
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1349 TTTCTGGTGCGCGTGCTGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCCTGGCGCGCATCG 1408
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                                                   GGCCGGACCGGCCGGCCAGCCAGCCAGCCAGCCGCCCACCGACCGGGTGTTGT
                                                                                                                                                                                       GACCGATGCTGGATCGTGCGTTGACGGTGCTCATCGACGCTCCCGAACCGCTTCCGGCAC 20955
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                                                                                     ACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAACGTTGGGGGGCAGACGTCGTCAAGC
                                                                                                                       CGCAGACGCCCGCGCCCGTACCCGATGTGCCCACGTGGGACTCGGTGGCGTGGCATCGCGCC
                                                                                                                                                       CTCCAACAACTCCTGGCGTGGCA---CTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTG
                                                                                                                                                                                                                         GTGCAGCGGTGGCAAAAACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTT 1231
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                                                                                                                                                                                                                                                                                                                               TTCTGGGACCACGGGTCTATGAGTTGCTCTATGGCGACCCCTTCCCATCCGGCGTCCAAA
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/transl_table=11
/product="probable_MONOOXYGENASE"
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/db_xref="GI:31617668"
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54.0%;
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Pred. No. 3.3e-60;
0; Mismatches 589;
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Search completed: November 13, 2003, 00:10:28 Job time: 7983.97 secs

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07-APR-2000;
03-AUG-2000;
The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lygine. The present sequence is a nucleic acid described in the exemplification of the invention.
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Tateishi
                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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AAF68082 and AAF68082 represent sequencing primers which are used in an example for the form the form of the form
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Best Local Sim:
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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Tateishi
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	GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC 56	ore 1473; DB 22; red. No. 0; Mismatches 0;	useful in animal feeds, in human medicine and in the pharmaceutical industry. Sequence 1473 BP; 275 A; 414 C; 456 G; 328 T; 0 other;	(4) a process for producing L-amino acids, comprising culturing a coryneform bacterium that overexpresses the accDA gene. Coryneform bacteria transformed with (I) so that they overexpress the accDA gene are useful for producing L-amino acids, especially L-lysine, which are	invention also describes (1) a polypeptide derived from (1) l lly defined 491 aa sequence; (2) coryneform microorganisms sformed with one or more copies of (1); (3) the shuttle vector coDA contained in Corynebacterium glutamicum DSM 12785; and	Disclosure; Page 12-15; 20pp; German. This invention describes a novel cloned Corynebacterium glutamicum DNA (I), replicable in coryneform microorganisms coding for an accDA gene	Cloned Corynebacterium glutamicum accDA gene useful for producing transformed coryneform bacteria producing increased yields of L-amino acids, especially L-lysine -	WPI; 2001-042411/06. P-PSDB; AAB45789.	(DEGS) DEGUSSA-HUELS AG. (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH. Tilg Y, Eggeling L, Eikmanns B, Sahm H, Moeckel B;	10-MAY-2000; 2000EP-0109842. 27-MAY-1999; 99DE-1024365.	EP1055725-A2. 29-NOV-2000.	Corynebacterium glutamicum.	C. glutamicum accDA DNA #2. L-amino acid; accDA; coryneform microorganism; L-lysine; animal feed;	15-MAR-2001 (first entry)	2733;	RESULT 5 AAC82733 Grandard DNA 1473 BD	1948 AGTCGCTTCACACGATTTGAGCGTTTAGCGCAG 1980
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Best Local Similarity
Matches 717; Conser
                                                                                                                                   This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polymucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
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                                                                                                                                                    The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37RV (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
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Note: The sequence data for this patent did not form specification, but was obtained in electronic format

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6294328B1	epidemiology, pacies	ields of	nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37Rv (AAI99682). The method is useful for evaluating strain variation of	sequence of the genome that correspond to positions in the complete	y deter	The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen,	Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.	esponding to positions where M. tuberculosis strains CDC $7Rv\ differ$ -	Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the	WPI; 2001-647261/74.	Fleischmann RD, White OR, Fraser CM, Venter JC;	(GENO-) INST GENOMIC RES.	24-JUN-1998; 98US-0103840.	24-JUN-1998; 98US-0103840.	25-SEP-2001.	US6294328-B1.	Mycobacterium tuberculosis.	Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.	Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.	15-JAN-2002 (first entry)	AAI99682;	RESULT 8 AA199682/c ID AA199682 standard; DNA; 4411529 BP.	1006831 CAGACGA 1006825	1874 TTGAAGA 1880	1006891 CGGCCGACCTACTGAAGTCGGGGATTGTCGACACCATCGTGCCGGAGTACCCCCGACGCCG 1006832	1814 CGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGGTCGTCGCCGAAACCGAGCACTTTG 1873	1006951 CGATCGTGTTCCGAGACACTGCTCATGCCGCCGAACTCGCTGCCGCCCAAGGCATCCGGT 1006892	1754 CCATCCTTTCCGCGACACCAACCACGCCGCGGAAATCATAGAGCGACAAGGCGTGCAGG 1813	1077 ALTOST CHARACTERS TO THE CONTROL OF THE CONTRO	1604 ************************************	1634 CCGTTTCGGTCATTATTGGTCAGGGCGTTGGCGGTGGCCATGGCCATGCTGGCCGCCG 1693	

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                                                                                TTGGGCCGCAGGAGCTGCGTTTTGCGCGCGTCGTGGCATTTCGCTGGCGCGCGAGCTAAAACC
                                                                                                                     GCGGCCAACCCACGGTGGTCCTCGGCCAGCAAAGGGCAGTAGGCGGCGGCGGAAGCACTG
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ilarity 54.0%;
Conservative
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Pred. No. 1.4e-82;
0; Mismatches 589;
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                                 This invention describes a novel nucleic acid array involving corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a ferentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent collumnations derived polynucleotides described in the disclosure of the
                                                                                                                                                                                       New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum -
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                                                                                                                                                             Claim 1; Page 154; 709pp; German.
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Sequence

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Best Local S
Matches 168
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                              Nakagawa
Tateishi
                                 analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                    The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. I are useful for identifying the mutation point of a gene derived from mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; amino organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C glutamicum
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                                                                                                                                                                                                   Claim 1;
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DB; AAG93188.
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                                                                                                                                                                                                   SEQ ID NO: 3442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 354
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Conservative
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Senoh A,
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2000JP-0280988.
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      The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in
                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                           Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001WO-US09180
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DB; AAU36304.
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; 2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
; 2000US-257931P.
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Pred. No. 2.2e-29;
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RESULT 12
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Best Local
                                                                                        10-OCT-2002
                                                                                                                                        Neisseria
                                                                                                                                                                Antibacterial; infection; vaccine; gene therapy; gene;
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Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
                                   12-FEB-2001; 2001GB-0003424
                                                                                                                WO200279243-A2
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52.8%;
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Pred. No. 1.2e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention.
 13-FEB-2002
                            AASS3191;
                                                     AAS53191 standard; DNA; 867
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                                                                                                                                                                                                                                                      The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wipo at
                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 259; Conser
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
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22-DEC-2000;
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DB; AAU35332.
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TTGTTTGAGCGGGCGACAGAAAAGCATTTACCAGTAGTGATTTTCACTGCATCTGGTGGT
                                                              ATGGACGCTAATTTATCATGGGCAGTATGGGAACGATTGTTGGTGAAAAAATCACACGC
                                                                                           TCCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAG
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; antibacterial; drug design.
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2000US-206848P.
2000US-207727P.
2000US-242578P.
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Xu HH;
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Pred. No. 4.3e-26;
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RESULT 14
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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAXI2938 to AAXI3919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcal.
                                                                                                                                                                                                                                                                                                            14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                      Claim 1; Page 1691-1694;
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RESULT 15
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ID ABS999XX
AC ABS99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animals, and for detecting E.faecalis usi present nucleic acid sequence represents DNA sequence of the invention.
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BG584921 EST486683
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BI725661 1031080C0
AG247247 Lotus jap
CB977199 CAB40003
AI222631 EST226326

BZ035752 Oeh49c05.
CB346970 CAB2SG000
CB081454 hk51h06.g
BZ051213 jnr62h07.
BH988285 Oej67b06.
BZ012471 Oed23c11.
BZ033778 Oed04001.
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BZ037784 lki53c01.
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BZ071328 lju13h07.
BH715901 BOHVJ644TR
BH462655 BOHUR54TF
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Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anopheles gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
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Other GSS: AG-ND-133C23.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                 Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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BZ026610 oeh27c06.
BH997475 oej71e06.
AQ991181 Rfc02065
BH994577 oei62f03.
AW587803 ST67B11 P
BH925341 odi46f02.
BZ579621 msh2 686.
BI725648 1031080B1

AU293522

Gardner, M.J.

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RESULT 2
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LOCUS
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Tel: 301 838 0708
Fax: 301 838 543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TICR). The BAC library was generated from A. gambiae PEST strain DNA, All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
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Seq primer: M13 For
Class: BAC ends.
                                                                                            sequence.
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/mol_type="genomic DN
/strain="PEST"
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/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1:
/86 c 109 g 156 t
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C. reinhardtii CC-1690 (mt+), CC-1691 (mt-), Gamete
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA
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Pred. No. 3.4e-14;
0; Mismatches 245; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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1 (bases 1 to 707)
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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Location/Qualifiers
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CTCGGCCATCCTCTCCGCGACACCCAACCACGCCGCGAAATCATAGAGGCGACAAGGCGT 1808
                                                                                                                                                                                                                                                                                                                                    GGAGCTGGGCCAGGGCGAGGCCATTGCCGTGAACCTGCGTGAGATGTTCGGCCTGCGTGT 465
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                                                                                            CGCCAACCGCAACCTGATCATGGAGAACGCGGTCTACTACGTGGCCTCGCCCGAGGCCTG 585
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Pred. No. 1.4e-13;
0; Mismatches 203;
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Query Match Best Local Similarity 48.8%; Matches 258; Conservative Qy 634 AATCAAGGCTATGCAGAGA Db 13 AATGATGATTATCAAAATC Qy 694 GTAATTACTGGAGAAGGCP Qy 694 GTAATTACTGGAGAAGGCP Db 73 GTTCAAACAGGCACAGGTC	/organism="Medicago library" /mol type="mRNA" /cultivar="medicago /db_xref="taxon:190 /clome="MHAM-7110" /clome="MHAM-7110" /tissue_type="roots /dev_stage="Roots h post-inoculation wit made from a mixture /lab host="E. coli (/clome lib="MHAM" /note="Vector: pBlue Xhol; cDNA was prepi roots harvested at j post-inoculation wit directionally ligate Stratagene and pack extracts. plasmids c extracts. plasmids c extracts. plasmids of the recombinant helper phage and pro 0RIGIN //organism="Medicago" /mol type="manual" /clome libe="MHAM" /clome	Contact: Harrison Plant Biology Divi The Samuel Roberts 2510 Sam Noble Par Tel: 580-223-5810 Fax: 580-221-7380 Email: mjharrison@ Other name: MHAM-7. Expressed Sequence available at http Seq primer: 73. Location/ ce	RESULT 3 AW584783 LOCUS DEFINITION N210917e MHAM Medicago trundling trun	Db 586 CGCCGCATCCTGTGGAAC Qy 1809 GCAGGCGCACGTTTT
4.0%; Score 84.2; DB 9; Length 604; imilarity 48.8%; Pred. No. 5e-13; ; Conservative 0; Mismatches 268; Indels 3; Gaps AATCAAGGCTATGCAGAGCCTTGGAGCGGGCTCGAAGCCAAATGCGATGAATCG	go truncatula/Glomus versiform go truncatula genotype A17" 19092" ts colonized with Glomus versi harvested at 10, 17, 22, 31 a with Glomus versiforme. The li re of RNA from each of these s i strain XLOLR" luescript SK-; Site_1: EcoRI; epared from polyA+ enriched RN t 10, 17, 22, 31 and 38 days with Glomus versiforme. The cD ared into the Unizap XR vector ckaged using Gigapack III Gold s containing cDNA inserts were ant lambda-Zap phage using Ex- propagated in XLOLR cells." g 194 t	more, OK 73401 more, OK 73401 te: 3/14/00; Updated to the EST) on 04/27/00; More info: e.tamu.edu/medicago'.	4 bp mRNA linear catula/Glomus versiforme pressiforme mixed EST libraters forme mixed EST libraters forme mixed EST libraters. H., Gonzales, M., Ellis, Lansen, T.S., Holt, L.E. and truncatula after coloniz	CGCCGCCATCCTGTGGAAGAGCCGCTCTGCCGCCGAGGCCACTGAGGCCCTGCGCGATGGCGCACTGTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGA 1859
Gaps 1; JAATCG 693 ATGCG 72 JATTTT 753 JATTTT 132	me mixed EST iforme" and 38 days ibrary was stages." Site_2: NA from DNA was t from DNA was d packaging de excised -assist	rmation is	mixed EST ary ary ary ary ary ary fraser,C.D., Fraser,C.M.	GCGCAT 645

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RESULT 4
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Contact: Michael A. Grusak
Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USF
Tel: 713-798-7078
Fax: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 773)
Grusak, M.A., Samac, D.A.,
,J. and Fraser, C.M.
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Medicago truncatula

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

Spermatophyta; Magnoliophyta; eudicotyledons; Trifolieae;

Spermatophyta; Magnoliophyta; eudicotyledons; Trifolieae;
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EST5313496 GESD Medicago truncatula cDNA clone pGESD15E20 5' end,
mRNA sequence.
BI311746
BI311746.1 GI:14986073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR sequence name: MTPAZ34TK
More information is available
seq primer: SKmod (CTA gAA CTA
Location/Qualifiers
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/db xref="taxon:3880"
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/tissue_type="immature seeds"
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/mol_type="mRNA"
/cultivar="A17"
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                Whole-Genome-Sequence variation among Psedomonas aeruginosa library J. Bacteriol., (2002) In press
                                                                                                                                                                                                 Pseudomonas aeruginosa
Pseudomonas aeruginosa
                                                                                     Spencer, D.H., Raymond, C.K., Smith, E.E., Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                       Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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ntact: Chris K.
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Pred. No. 1.7e-12;
0; Mismatches 269;
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Best Local Sim
Matches 206;
             TITLE
JOURNAL
                                                               AUTHORS
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University of Washington
Box 352145, Seattle, WA 99
Tel: 2062216954
Fax: 2066657244
                                                                                            Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
             ESTs from developing 
Unpublished
                                                             Grusak, M.A.,
                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                             BI310727 712 bp mRNA linear EST 20-JUL-2001
                                                                                                                                                                            Medicago truncatula (barrel medic)
                                                                                                                                                                                                              BI310727.1
                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: craymond@u.washington.edu Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGATGCCGATCCTCACCTTCATCGACACGCCCGGCGCCTACCCGGGGGATCGATGCCGA
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                                                                                                                                                                                                                                                                                                                                                                CACCGCCGAGCGCCTGAAAGGCCTGGGCATCGTCGACAAGGTCATCGACGAACC 471
                                                                                                                                                                                                                                                                                                                                                                                           GCAGGCGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAAC 1862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCGACCAGTTGAACATGCTGCAATACTCCACCTATTCGGTGATCTCGCCGGAAGGATG
                                                                           (bases 1 to 712)
                                               and Fraser, C.M.
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Michael A.
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/clone_lib="pacs1-60"
/note="clinical isolate 1-60
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                                                             Samac, D.A.,
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                             reproductive tissues of
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Pred. No. 5.2e-12;
0; Mismatches 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     754 TCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baylor College of Medicine
1100 Bates Street, Houston,
Tel: 713-798-7044
Fax: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: SKmod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USDA/ARS Children's Nutrition Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             More information is available at:
Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
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                                                                                                                                                                                                            CGCGAGGCGCATTTGCCGTTTCCTGGTGTATTTGCGCAA---TCCCCACGATGGGTGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTCAAACAGGCACAGGTCAAGTAAATGGTATTCCTGTAGCAATAGGTATTATGGATTTT
TTTGCAGGTAAAAGAGTAATTGAAGAAACGTTGAAGATCGAAGTGCCCGAAGGTATACAA
                                       TTCCTGGGTCCTCGCGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAG 1110
                                                                                  ACAGCTAGTTTTGGAATGTTGGGGGATATCATTCTTGCCGAACCCGATGCTTACATAGCA
                                                                                                                            ATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGT 105
                                                                                                                                                                      CAAATCAATCAAAAGTTATTCTATGTACCGATACTTACATCTCCTACTACTGCTGGGGGTA
                                                                                                                                                                                                                                                      CAAGAAGGAAGTTTGAGCTTAATGCAAATGGCTAAAATTTCTGCTTCTTTATATAATTAT
                                                                                                                                                                                                                                                                                                                                        TATGCTACCAATCAACGTTTACCTCTTATTATAGTATGTGCGTCTGGAGGAGCGCGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                             AATGATGATTATCAAAATCGTCTTGATTCTTATCAAGACAGAACTGGATTACTGGATGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA-enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phage using XLOLR cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="immature seeds"
/dev_stage="Immature seeds, 1
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collected from pods ranging in a
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More information is available at: www.medicago.org
Seq primer: SKmod (CTA 9AA CTA 9tg 9AT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1100 Bates Street, Houston,
Tel: 713 798 7044
Fax: 713 798 7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Grusak, M.A.
USDA/ARS Children's Nutrition Research
Baylor College of Medicine
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Cheung,F. and Fraser,C.M.
More ESTs from developing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mgrusak@bcm.tmc.edu
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GATTTTGAGTTTATGGGAGGTAGTATGGGATCCGTAGTGGGTGAGAAAATCACTCGGTTG
                                      GATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCG 807
                                                                                 GATGCGGTTCAAACAGGCACAGGTCAAGTAAATGGTATTCCTGTAGCAATAGGTATTATG 61
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                                                                                                                                                                                                                                                                                     171
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       /note=Tyector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in age from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. CDNA was prepared from polyA+enriched RNA. The CDNA was directionally ligated into
                                                                                                                                                                                                                                                                                                     enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="Immature seeds, 11 to
pollination"
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/mol_type="mRNA"
/cultivar="A17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone_lib="GESD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="immature seeds"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glomus versiforme, 2001
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Sam Noble Parkway, Ardmore,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mjharrison@noble.org
/clone lib="MHAM"
/clone lib="MHAM"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
EcoRI; Site 2:
/note="Vector: pBluescript Sk-; Site 2: EcoRI; Site 2: EcoRI; Site 2:
/note="Vector: pBluescript Sk-; Site 2: EcoRI; Sit
                                                                                                                                                                       /tissue_type="roots colonized with Glomus versiforme"
/dev stage="Roots harvested at 10, 17, 22, 31 and 38 post-inoculation with Glomus versiforme. The library made from a mixture of RNA from each of these stages.
/lab host="E. coli strain KLOLR"
                                                                                                                                                                                                                                                                                                          clone="pMHAM-20E21"
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'cultivar="Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Medicago truncatula/Glomus versiforme
                                                                                                                                                                                                                                                                                                                                    xref="taxon:119092"
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Contact: Chris K.
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Spencer,D.H., Raymond,C.K., Smith,E.E.,
Burns,J.L., Kaul,R. and Olsen,M.V.
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GSS.
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/organism="Pseudomonas
/mol_type="genomic DNA"
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                                                                                               Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Eukaryota; Chlamydomonas.
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Lambda Zap II |
BI725661
                                                                                                                                                                  Unpublished
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                 Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulativascular Plants. Project: 1031
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                                                                                    chauser@duke.edu.
organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
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/db xref="taxon:287"
/db yref="taxon:287"
/clone="pacs2-164"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic
                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library."
                                                                                                                                                                                                                                                                                                                                                                                                                               C. reinhardtıı
Chlamydomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                  539 bp mRNA lii
reinhardtii CC-1690, Stress:
lamydomonas reinhardtii cDNA,
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2.6e-11;
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90, Stress II (normalized),
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ORIGIN
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Best Local Similarity
                                                                                                                                                                                          1749
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TCACCTCGGCCGAGCTGGAGGTGAAGTTCGGCGTCATGGACCACATCGTGCCGGA
                                                                                                                                                                                       CTCGGCCATCCTCTTCCGCGA-CACCAACCACGCCGCGGAAATCATAGAGCGACAAGGCG 1807
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                                                        TGCAGGCGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGA 1859
                                                                                                                           CGCCGCCATCCTGTGGGAAGAGCCGCTCTGCCGCCGGCGAGGCCACTGAGGCCCTGCGCA
                                                                                                                                                                                                                                                      CGCCAACCGCAACCTGATCATGGAGAACGCGGTCTACTACGTGGCCTCGCCCGAGGCCTG
                                                                                                                                                                                                                                                                                                                      CGCCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGC 1748
                                                                                                                                                                                                                                                                                                                                                                                  GGAGCTGGGCCAGGGCCATTGCCGTGAACCTGCGTGAGATGTTCGGCCTGCGTGT
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Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
synthesized. The DNA was directionally cloned into lambda
synthesized. The Boori (5') and XhoRI (3')
sites. pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
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/clone lib="C. reinhardtii CC-1690,
), Lambda Zap II"
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51.0%;
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Pred. No. 2.3e-11;
0; Mismatches 201;
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RESULT 11 AG247247 REFERENCE AUTHORS DEFINITION ACCESSION VERSION REFERENCE FOCUS KEYWORDS ORGANISM TITLE JOURNAL Lotus japonicus
Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vardiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus japonicus TAC End sec Published Only in Database 2 (bases 1 to 652) GSS. Lotus japonicus AG247247 AG247247.1 GI:2 Sato, S., Nakamura, Y. AG247247 GI:26647012 DNA, clone:LjT20k03_not, genomic survey sequence. and Tabata, S 652 ď DNA GSS 13-DEC-2002

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RESULT 12
CB977199/c
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                                                                                          REFERENCE
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TITLE
                                                            AUTHORS
   TITLE
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                                                         Goes
                                                                                                                                                                                                                                                                                                                       617 bp mRNA linear CAB40003 IVa Ra D11 Cabernet Sauvignon Berry - CAB4 cDNA clone CAB40003_IVa_Ra_D11 3', mRNA sequence. CB977199
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Direct Submission

Direct Submission

Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,

Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,

The First Laboratory for Plant Gene Research; 2-6-7

Kazusa kamatari, Kisarazu, Chiba 292-0818, Japan

(B-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,

Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
                                                                                    Spermatophyta; Magnoliophyta; Vitaceae; Vitis.
1 (bases 1 to 617)
                                                                                                                                                                   Vitis vinifera
Eukaryota; Viridiplantae;
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
                                                                                                                                                                                                                                      Vitis vinifera
                                                                                                                                                                                                                                                                                            CB977199.1 GI:30300405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTTGGTGAAAACTG 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCTCACTTTTGCGGAAACCCGGCGCGCGGATAGGTTTCCTGGGTCCTCGCGTGGTGGAGT 107:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCAATCCTTACATCTCCCACTACTGGTGGGGTAACAGCTAGTTTTGGCATGTTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTATTTGCGCAA---TCCCACGATGGGTGGCGCCATGGCCTCGTGGGGTTCATCTGGGC 1015
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                                                         da Silva, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/clone_lib="genomic TAC library"
/note="VECTOR.PYLTAC7"
107 c 129 g 218 t
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(mol_type="genomic DNA"

(strain="Miyakojima MG-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
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                                                      Iandolino, A., Lim, H.,
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Pred. No. 4.5e-11;
0; Mismatches 219;
                                                                                                                                           Streptophyta; Embryoyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             515
                                                      Baek, J., Jones, K. and
                                                                                                                                                                            Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                              eudicots;
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UC Davis, Plant Pathology
One Shields Ave, Davis, CA 9
Tel: 530 754 6561
Fax: 530 754 6617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250;
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Contact: Douglas Cook,
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   GGTAAAAGGGTAATTGAACAAACATTGAAAAAAGACAGTACCTGAAGGGTTCACAAGCGGCT
                                                      GETCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCG 1116
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//clone | lib=|Cabernet Sauvignon Berry - CAB4"

//clone | Serry; Vector: pDNR; Site | 1: Sfi; Site_2:

Sfi; CAB4 is a cDNA library of Vitis vinifera cv.

/Cabernet Sauvignon' Clone B berries. Sampled berries were collected from field-grown vines during stage II of berry growth (berries were green and hard) at approximately 60 days after full bloom. The average berry size was 9 milimeters. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5'and 3' adaptors were used in cloning as follows:

5'-AMCCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and constructed using the Clontect Creator SMART wit and size-selected to contain the 0.5-3 kb size fraction."
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/clone="CAB40003 IVa Ra_D11"
/sex="Hermaphrodite"
/dev stage="Berry on stage II,
/lab_host="DH5alpha"
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/mol_type="mRNA"
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0; Mismatches 270;
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The Institute for Genomic Re
9712, Medical Center Drive,
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EST226326 Normalized rat embryo,
REMCJ63 3' end, mRNA sequence.
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Lee,N.H., Glodek,A., Chandra,I., Mason,T.M.,
Kerlavage,A.R. and Adams,M.D.
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Mammalia; Eutheria;
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                                                                                                                                                              TGTCGCTGATGCAGATGGCGAAAACCTCTGCGGCACTGGCAAAAATGCAGGAGCGCGGCT
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(301)-838-0208
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/mol Lype="mRNA"
/db_xref="ATCC (inhost):2036524"
/db_xref="taxon:10118"
/clone="REMCJ63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Nembryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pTTT1Pac; Site_1: EcoRI; Site_2: NotI"
/note="Vector: pTTT1Pac; Site_1: EcoRI; Site_2: NotI"
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1055 TGGGTCCTCGCGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGG 1114
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1 (Dases 1 to 677)

Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   washington University School of Email: submissions@watson.wustl. Plate: oeh49 row: c column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence start: 8
High quality sequence stop: 551
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28RPpOT reverse Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole genome shotgun reads from Brassica oleracea Unpublished
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                                CAAGTTTTGGTATGTTGGGGGATATCATTATTGCCGAACCCTATGCCTACATTGCATTTG 123
                                                                                                      CAAGTAAAAAGGTATTCTATATATCAATTCTTACATCTCCTACTACCGGTGGGGTGACAG
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                                                                   CCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGGCGCAGATAGGTTTCC
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/note="Vector: pOTw13; whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
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482 TATTTATTCCATAAGGGCTTATTCGATCTAATCGTACCAC 521
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Search completed: November 13, 2003, 02:26:29 Job time: 4682.43 secs

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Result
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1: /ggn2_6/ptodata/2/ina/5A_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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3 4 US-09-362-899-1
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   ; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Corynebacterium g: FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1473)
; OTHER INFORMATION: accDA
US-09-362-899-2
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                                                                                                                                                                                                  Sequence 2, Application Patent No. 6361986 GENERAL INFORMATION:
                                                                                                           APPLICANT: Degussa-Hls AG
APPLICANT: Forschungszentrum-Jlich GmbH
TITLE OF INVENTION: PROCESS FOR THE PREPARATION
CURRENT APPLICATION NUMBER: US/09/362,899
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: DE 19924365.4
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 3
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches
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RESULT 3

US-09-103-840A-2/c

Sequence 2, Application US/09103840A

Patent No. 6294328

GENERAL INFORMATION:
APPLICANT: PLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILLING DATE: 1998-06-24
RUMBER OF SEQ ID NOS: 2
                                                                                                                                                                 US-09-103-840A-2
                                                                            Query Match
Best Local Similarity
Matches 717; Conserva
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn SEQ ID NO 2
                                                                                                                                                                              ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at vario
OTHER INFORMATION: represent a, t, c
                                                                                                                                                                                                                                                                                        LENGTH: 4403765
TYPE: DNA
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                                      ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC
ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG
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                                                                                                 14.7%;
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                                                                            Score 312.6; DB 3;
Pred. No. 2.7e-80;
0; Mismatches 589;
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CGATCGTGTTCCGAGACACTGCTCATGCCGCCGAACTCGCTGCCGCCCAAGGCATCCGGT 1006892
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                                                     CCATCCTCTTCCGCGACACCAACCACGCCGCGAAATCATAGAGCGACAAGGCGTGCAGG
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; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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APPLICANT: FLEISCHMAN, Robert
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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                                                                                             TGGCCTCGTGGGGTTCATCTGGGGATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGTT
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   TTCTGGGACCACGGGTCTATGAGTTGCTCTATGGCGACCCCTTCCCATCCGGCGTCCAAA
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Pred. No. 2.7e-80;
0; Mismatches 589;
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                                                                                                                                                                                             Sequence 140, Application US/08311731A Patent No. 6583266
                                         ENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS
TITLE OF INVENTION: DIACKOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES; 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
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US-08-311-731A-140
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Best Local Similarity
Matches 296; Conserv
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
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MOLECULE TYPE: DN
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02210
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TOPOLOGY: circular
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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GGACTGCAACTGACGTTGAATCGTGCGCTGACGATGAT 31940
                                                 CAATTGCGTGCAGCGGTGGCAAAAACCCTCAAGGTTAT 1202
                                                                                                                                                                                                                                  ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT 1104
                                                                                                                                                                                                                                                                                                                                        GGCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCGCAG 1044
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                                                                                                   ATCCAGACAGCGGAGAATCTGCAACGGCATGGGGTAATCGACGCTATCGTCACGCTGGAC
                                                                                                                                                   ATCGGCTTCCTTGGGCCTCGGGTGTATGAGTTGCTGTATGGCGAACCTTTCCCGTCCGAC
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12180
LENGTH: 1020
TYPE: NUMBER OF SEQ ID NOS: 35142
                                                                                                                                                         RESULT 7
US-09-252-991A-12415/c
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                                                                                                                         Sequence 12415, Application Patent No. 6551795
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                                                                                                      GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM: Pseudomonas aeruginosa
-09-252-991A-12180
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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Pred. No. 2.7e-24;
0; Mismatches 241;
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                                                                  APPLICANT: Khosla, Chaitan
TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-1
TITLE OF INVENTION: AUTAGONISTS
FILE REFERENCE: 28600-20210.00
CURRENT APPLICATION NUMBER: US/09/773,816
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1
                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 23673
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09773816 Patent No. 6340774
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       TYPE: DNA
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ESTROGEN-RECEPTOR

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US-09-252-991A-12415
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PRIOR FILING DATE: 198-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12415
LENGTH: 1338
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ORGANISM: Pseudomonas
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AGTTGCGGCCGCCCTGGCCAA 176
                                        AATTGCGTGCAGCGGTGGCAAA 1187
                                                                                                                                                             TCGGCTTCGCCGGTCCCCGCGTGATCGAGCAGACCGTCCGCGAGAAGCTGCCGGAAGGCT
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                                                                                                                        Conservative
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Pred. No. 3.1e-24;
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(23623)
OTHER INFORMATION: n = A,T,C
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Pred. No. 2.7e-21;
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GENERAL INFORMATION:
                                                                                                                                                                                                                              TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 170:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TOPOLOGY: circular MOLECULE TYPE: DNA (genon HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 870 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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CORRESPONDENCE ADDRESS
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TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
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                                                                                                                               STRANDEDNESS: double
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SOFTWARE: ASCII
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COUNTRY: USA
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and David Bush AND AMINO ACID SEQUENCES RELATING FAECIUM FOR DIAGNOSTICS AND THERAN

THERAPEUTICS

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7307 1913

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INAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...8;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-107-532A-170
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US-09-252-991A-12365/c
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                                                                US-09-252-991A-12365
                                                                                                                          SEQ ID NO 12365
                                                                                                                                                                                                                                                                                                                                     Sequence 12365, Application US/09252991A Patent No. 6551795
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Best Local
                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-17,788
PRIOR FILING DATE: 1998-07-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEC. 1998-07-27
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 Matches
                             Query Match
                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                              TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                LENGTH: 444
TYPE: DNA
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Pred. No. 1e-20;
0; Mismatches 2
             Score 97.2; DB 4;
Pred. No. 8.2e-19;
 Mismatches
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US-08-961-527-7/c
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Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
                                                     TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                           NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE. ASCIL Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                        TELEPHONE: (301) 309-8512
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 42
LENGTH: 19702 base
TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville
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                                                                                                              (301) 309-8504
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RESULT 12
US-09-557-884-1
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09557884

Patent No. 6506581

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of the Hamman of the Hamman influenzae
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Best Local
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                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION NOMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: Unknown>
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                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                        PRIOR
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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   APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                       STATE: MD
                                                                                                                                                                                                                                                                        STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTACCAGATACGATTGCTA 11053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTGCGTGCAGCGGTGGCAA 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGT
                                                                                                                                                                                                                      ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCAAAAGGCAGAATTCCTATTAGAACATGGCTTTGTGGATGCTATTGTCAAAAGAAGAG
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Pred. No. 1.1e-17;
0; Mismatches 253;
                                                                                                                                                                                                                                                                                                                                                               and Uses Thereof
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US-09-643-990A-1
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GENERAL INFORMATION:
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Best Local (
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NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
ADDRESSEE: Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
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TYPE: nucleic acid
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REGISTRATION NUMBER: 41,971
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Owen White
Hamilton O. Smith
J. Craig Venter
OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd
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Human Genome Sciences,
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Pred. No. 1.2e-16;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-643-990A-1
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FILING DATE: 1995-06-07
APPLICATION UMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: KENLEY K. HOOVET
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEPHONE: 301-610-5790
TELEPHONE: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
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Best Local
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MEDIUM TYPE: 3 1/2 inch disket/
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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AATTGCGTGCAGCGGTGGCAA 1186
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                                                                  TCCAACGTAGTGAGTTTCTACTTGAGAAAGGGGCAATTGATATGATCGTGAAACGTTCAG 1337459
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STRANDEDNESS: double
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FILING DATE: 23-Aug-2000
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Pred. No. 1.2e-16;
0; Mismatches 253;
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US-09-347-878-25
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Best Local Similarity
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TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: M32445/GenBank
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LOCATION: (1131)
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                           TAGTGGTACCCCCGGTACCGGA 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAGGCGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTCTTTGGGCACGGTCGCGTGCGCATCATGAAGGCGATTCACCGCGCCACAGAGC 826
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                                                                    GCGTGGCACTTCCGGTGATGGA 1268
                                                                                                                                                                                                                                                                                                                                                                               TGCTGGGCGATCTCAACATCGCTGAACCGAAAGCGTTAATGGCTTTGCCGGGTCCGCGTGT 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCATGGCCTCGTGGGGTT 1006
                                                                                                                                                                                                    TCGAGAAAGGCGCGATCGACATGATCGTCCGTCCGCGAAATGCGCCTGAAACTGGCGA
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                                                                                                           GCATTCTGGCGAAGTTGATGAATCTGCCAGCGCCGAATCCTGAAGCGCCGCGTGAAGGCG
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US-08-973-275-2
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CURRENT FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: PCT/JP97/01043
EARLIER FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: JP 8-97536
EARLIER APPLICATION NUMBER: JP 8-97536
EARLIER FILING DATE: 1996-03-28
EARLIER APPLICATION NUMBER: JP 8-146833
EARLIER FILING DATE: 1996-05-16
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.1
Best Local Similarity 33.6
Matches 152; Conservative
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SEQ ID NO 2
LENGTH: 954
TYPE: DNA
ORGANIEM: Magnetospirillum AMB-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MATSUNAGA, Tadashi
APPLICANT: MAMIYA, Shinji
APPLICANT: MAMBA, Kenryo
TITLE OF INVENTION: FINE MAGNETIC PARTICLES CONTAINING USEFUL PROTEINS
TITLE OF INVENTION: BOUND THERETO, PROCESS FOR PRODUCING THE SAME, AND USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: MATSUNAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEATURE:

NAME/KEY: gene
LOCATION: (217)...(702)

OTHER INFORMATION: Predicted region encoding membrane bound portion
OTHER INFORMATION: of the mps gene product. "n" is any of a, t, c or
OTHER INFORMATION: g.
                                                                                                                            1698 GGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCTCGGCCAT 1757
                                                                                                                                                                                                                                                                                                                                                                                                      1638 TTCGGTCATTATTGGTCAGGGCGTTGGCGGTGGCGCGCTGGCCATGCTGCCCGCCGATCT 1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1518 GATCGTGTCCATCATCGACACCTCCGGCGCGCGAATTGTCGCAGGCGCGGCTGAGGAGCTCGG 1577
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813 YMGNAAYCCNGAYYTNATGATGCARACNYTNWS
                                                                                                                                                                                                                                                                  633 NGTNYTNATGYTNGARCAYGCNATHTAYWSNGTNATHWSNCCNGARGGNTGYGCNWSNAT
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                                       AGAAATTCTCGGCACAATCAGCAACGCCCTCTC 1910
                                                                                  RGAYYTNCAYAARYTNWSNATHATHGAYWSNGTNGTNCCNGARCCNATGGGNGGNGCNCA
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33.6%; Pred. No. 9.4e-16;
ative 54; Mismatches 247;
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Search completed: November 13, 2003, 00:14:44

Job time : 166.654 secs



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Result
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Maximum DB
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seq length: 2000000000
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Match Length DB
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Gapop 10.0 , Gapext 1.0
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               0 10 US-09-738-626-1

10 US-09-738-626-929

13 US-10-024-370-2

10 US-09-712-363-35

10 US-09-815-242-7800

9 US-09-815-242-6828

10 US-09-815-242-7288

10 US-09-815-242-7288

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Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 35, Appl
Sequence 341, Appl
Sequence 7800, Ap
Sequence 6828, Ap
Sequence 6828, Ap
Sequence 7458, Ap
Sequence 97, Appl
Sequence 97, Appl
Sequence 984, Ap
Sequence 9850, Ap
Sequence 9530, Ap
Sequence 5531, Ap
Sequence 5531, Ap
Sequence 57115, Ap
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44.4	44.8	45	45.8	46	46.2	48.2	48.6	48.6	49.8	49.8	49.8	52.6	54.6	56.4	57.2	59.6	59.6	67.8	67.8	79	79	81.8	84.8	85.2	86.4	93	96.2
2.0	2.1	2.1	2.2	2.2	2.2	2.3	2.3	2.3	2.3	2.3	2.3	2.5	2.6	2.7	2.7	2.8	œ	'n	'n		7	·	4.0	4.0	4.1	4.4	5
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12 US-10-162-497-7 12 US-10-289-757-151			9 US-09-815-242-4026	9 US-09-841-132-461		9 US-09-767-479-11	14 US-10-156-761-3330	9 US-09-815-242-2856		9 US-09-815-242-9521	9 US-09-815-242-9268	9 US-09-815-242-9799	ج.			9 US-09-815-242-3909	9 US			14 US-10-156-761-1		9		9 US-09-815-242-4369	9 US-09-815-242-8520	9 US-09-815-242-9267	14 US-10-329-960-1
Sequence 7, Appli Sequence 151, App	Sequence 7101, Ap	Sequence 2173, Ap	Sequence 4026, Ap	Sequence 461, App	Sequence 14, Appl	Sequence 11, Appl	Sequence 3330, Ap	Sequence 2856, Ap	Sequence 3349, Ap	Sequence 9521, Ap	Sequence 9268, Ap	Sequence 9799, Ap	Sequence 5951, Ap	Sequence 269, App	Sequence 1085, Ap	Sequence 3909, Ap	Sequence 6829, Ap	Sequence 1, Appli	Sequence 3318, Ap	Sequence 1, Appli	5702		312,	4369,	Sequence 8520, Ap	Sequence 9267, Ap	Sequence 1, Appli

ALIGNMENTS

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PRIOR APPLICATION NUMBER: 09/362,899
PRIOR PILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: DE 199 24 365.4
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2123
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: gene
; LOCATION: (508)..(1980)
; OTHER INFORMATION: accDA
US-10-024-370-1
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APPLICANT: TILG, YVONNE
APPLICANT: ELKMANNS, BERND
APPLICANT: EGGELING, LOTHAR
APPLICANT: SAHM, HERMANN
                                                                                             Query Match 100.0%; Score 2123; Best Local Similarity 100.0%; Pred. No. 0; Matches 2123; Conservative 0; Mismatches
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MOCKEL, BETTINA
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY
TITLE OF INVENTION: FERMESVIATION AND NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: accda Gene
FILE OF INVENTION: accda Gene
FILE REFERENCE: 21123-284139-MAS
CURRENT APPLICATION NUMBER: US/10/024,370
CURRENT FILING DATE: 2001-12-21
CURRENT FILING DATE: 2001-12-21
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CTCGAGCGGGAGTCGGTGATCGGCCACTCTCTAAGCAATGCCGGCTTTAAAATAAAGCAA
                                                                                                                                             DB 13;
                                                                                             0
                                                                                                                                          Length
                                                                                                                                             2123;
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1081 ACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTGGTGAAAACTGGTGTG 1140 	1021 ACTITICGGAACCCGGCGCAGATAGGTTTCCTGGGTGCTCGAGTTGATCTGGGAGTTAACC 1080 1021 ACTITICGGAACCCGGCGCAGATAGGTTTCCTGGGTCCTCGCGTGGAGTTAACC 1080 1021 ACTITICGGAACCCCGCGCAGATAGGTTTCCTGGGTCCTCGCGTGGAGTTAACC 1080	1 ATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTG 9	781 GTCGCGTCGGTGCGCATCATGAAGGCGATCACGCGCCACAGAACTGAACTCCCACTG 840 841 CTGGTCTCCCCTGCTTCCGGTGGTGCGCGCACAGAAAAACAAATCGAGCTTTTGTCATG 900	721 GGCATTCCGGTAGCCGTTATTTTGTCCGATTTTTCCTTCC	61 CGGGCTCGAAGCAAGGCCAAATGCGATGAATCGGTAATTACTGGAGAAGGCACCGTGGAG 72 	01 TCTTGGAATGAAACTCCCCAATATGACAACCTCAATCAAGGCTATGCAGAGACCTTGGAG 6	41 ATGGAACACTTCAGCATTGACGCTCATAGACTCGGTTTTTGGACCCTGACAGCTTCATT 6 A TIGGAACACACTTCAGCATTGACGCTCATAGACTCGGTTTTTTGGACCCTGACAGCTTTCATT 6	ATTAATTAACAAAGCCATTTTTCGGCCGTGGAGAAGCGTTTTCCGACTATGGTGTGGGGC 5	21 TCGATAGCCTAAATTGGGCTTAGATCTTCCGCCTCTAAATAGGTATGCAGAGACACTTCGA 4	61 ACGTCTAGGCAAAAAGTAGTTTTGTGAGATGAAAACGCATAATCCGTCATTTTTTTT	GTGCAATAGTTAACGGGCTTCACACGTCACCATTCTGTCCGGTTTTAGGCTATGTTCGGG 3	TCCCGATCTACCCCCTCTTTACCCCGAAATACCCCCTTTTGCAAAGATTGCAAACACAACA 3	181 ACTCCCCCCAATATCTTAAACTTAAAACTTACAATTTTTT	AACGTGTGAATGTGAAGTTACCTAACTCACATTGCAATGCGATAGCGATTTGGAAAACTC 1	61 CTTATATGTTTCTCACCACATCTGGCCGACGACGACGAAGTATGTTGTCGATCACAGCTA 120
RESULT 2 US-09-738-626-1/c US-09-738-626-1/c ; Sequence 1, Application US/09738626 ; Publication No. US20020197605A1	Db 2041 GTGGCCGGAACCCTTCATGCCTGAAGCAGCCTCTGGCGGAATGGTCAGCTGACGACGTCC 2100 Qy 2101 GCCGACCTTCATGCCTGGAATTC 2123 Db 2101 GCCGACCTTCATGCCTGGAATTC 2123	OY 1981 TAAAGAAANTTATGCGCTGATCAAATCGATGATGAACACCAGGGTACGGCCAGACAGTGG 2040		QY 1801 CAAGGUGTGCAGGCACTITIAAGCCAAGGGTTAATGCAGGGATGGTCGACGAA 1800	1741 GAGGGCGCCTCGGCCATCCTCTCCGCGACACCAACCACCCGCGGAAATCATAGAGCGA	Qy 1681 ATGCTGCCCGCCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCA 1740	Qy 1621 GCTCCCCTCCCCACCGTTTCGGTCATTATTGGTCAGGCCGTTGGCGGTGGCGCGCTGGCC 1680	Qy 1561 GCGGCTGAGGAGCTCGGCATCGCAAGCTTGCGCGCACCTTGTCCAAGCTTATCGAC 1620	Qy 1501 CGCGAGCTAAACCTGCCGATCGTGTCCATCATCGACACCTCCGGCGCGCGAATTGTCGCAG 1560	OY 1441 CGCCGCTTCACGCTTGGGCCGCAGGAGCTGCGTTTTGCGCTGGCATTTCGCTGGCG 1500	Qy 1381 GCTGTGCGCCTTGCCCTGGCGCCCATCGGGGGCCCGTGGTGCTGATTGGGCAGGAT 1440	Qy 1321 GAAACGTTGGGGGCAGACGTCGTCAAGCTTTCTGGTGCGCGTGTGGCGCATTGAGCCCG 1380	OY 1261 GTGATGGAGGCGATTGCGCGTTCTCGTGACCCGCAGAGGCCTGGAATCGGGGAGATTATG 1320	Qy 1201 ATTCAGCCGGTAGAGGCAACGGATCGTTTTTCTCCAACAACTCCTGGCGTGGCACTTCCG 1260	OY 1141 ATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAGCGGTGGCAAAAACCCTCAAGGTT 1200

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APPLICANT: ANDO, SHING
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILLE REFERENCE: 249-125
FILLE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP-94/377484
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
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Best Local Similarity 100.
Matches 2122; Conservative
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ANDO, SEIKO
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                                   GCTCCCCCCACCGTTTCGGTCATTATTGGTCAGGGCGTTGGCGGTGGCGCGCTGGCC
                                                       GCTCCCCTCCCCACCGTTTCGGTCATTATTGGTCAGGGCGTTGGCGGTGGCGCTGGCC
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Query Match 69.4%; Score 1473; DB 10; Length 1473; Best Local Similarity 100.0%; Pred. No. 0; Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 508 GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC 567	R OF SEQ ID NOS: 7059 ARE: PatentIn ver: 3.0 NO 929 IH: 1473 : DNA NISM: Corynebacterium glu 3-626-929	ENT APPLICATION APPLICATION APPLICATION ATT FILING DATE: APPLICATION I APPLICATION I APPLICATION I APPLICATION I APPLICATION I	APPLICANT: HAYASHI, MIKIKO APPLICANT: YOKOI, HARUHIKO APPLICANT: YOKOI, HARUHIKO APPLICANT: TATEISHI, NAOKO APPLICANT: IKEDA, MASATO APPLICANT: IKEDA, MASATO APPLICANT: OZAKI, AKIO TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES	-929 9, Applicat No. US2007 ORMATION: NAKAGAWA, MIZOGUCHI ANDO, SEI	Db 879581 GTGGCCGGAACCCTCAGGGCCGTAAGCAGCCTCTGGCGGAATGGTCAGCTGACGACGTCC 879522 Qy 2101 GCCGACCTTCATGCCTGGAATTC 2123	Db 879701 ACAATCCGACAGCCGGGACCGGCACCAGTCCCAGGCGAATTCGACGCCAGACGTCC 2040 Qy 1981 TAAAGAAATTATGCGCTGATCAAATCGATGATGATGAACACCAGGGTACGGCCAGACAGTGG 2040	Qy 1861 ACCGAGCACTTTGATGAAGAAATTCTCGGCACAATCAGCAACGCCTCTCCGAATTGGAT 1920	QY 1741 GAGGGGCCTCGGCCATCCTCTCCGGACACCACCCACCGGAAATCATAGAGGA 1800 1741 GAGGGGCCTCGGCCATCCTCTCCGCACACCACCCACCCGCGGAATCATAGAGGA 1800 1879881 GAGGGCGCTCGGCCACTCTTCCGCGACACCACCCACGCCGGGAATCATAGAGGCA 879822 1801 CAAGGCGTGCAGGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAA 1860 1	879941 ATGCTGCCCGCCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCA
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Query Match Best Local Similarity 100.0%; Pred. NO. 0; Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 508 GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACTTCAGCATTGACGCTC 567	PRIOR FILING DATE: 1999-07-29 NUMBER OF SEQ ID NOS: 3 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2 LENGTH: 1473 TYPE: DNA ORGANISM: Corynebacterium glutamicum FEATURE: NAME/KEY: CDS LOCATION: (11(1473) OTHER INFORMATION: accDA S-10-024-370-2	RESULT 4 US-10-024-370-2 ; Sequence 2, Application US/10024370 publication No. US20020142405A1 ; GENERAL INFORMATION: ; APPLICANT: TILG, YVONNE ; APPLICANT: ELKMANNS, BERND ; APPLICANT: ECSCELING, LOTHAR ; APPLICANT: MOCKEL, BETTINA ; ITTLE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY ; TITLE OF INVENTION: GENERAL GENE ; TITLE OF INVENTION: ACCDA GENE ; TITLE OF INVENTION: accDA GENE ; FILE REFERENCE: 21123-284139-MAS ; CURRENT APPLICATION NUMBER: US/10/024,370 ; CURRENT FILING DATE: 1909-07-29 ; PRIOR APPLICATION NUMBER: 09/362,899 ; PRIOR PILING DATE: 1999-07-29 ; PRIOR APPLICATION NUMBER: 09/362,899	Qy 1948 AGTCGCTTCACACGATTTGAGCGTTTAGCGCAG 1980	OY 1828 AGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTC 1887	Qy 1708 GCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCTCGGCCATCCTCTTCCGC 1767	Db 1141 ATTGGTCAGGCGTTGGCGGTGGCGCCGCCATCTGGTCTACGCG 1200
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TYPE: DNA
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CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
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APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DITERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
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APPLICANT: Rotstein, Sergio
APPLICANT: Marcotte, Edward
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SOFTWARE: FastSEQ for Windows Version
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OR FILING DATE: 2000-02-01
OR APPLICATION NUMBER: 60/117,844
OR FILING DATE: 1999-01-29
OR APPLICATION NUMBER: 60/118,206,
OR FILING DATE: 1999-02-01
OR APPLICATION NUMBER: 60/126,593
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                   CGGCCGACCTACTGAAGTCGGGGATTGTCGACACCATCGTGCCGGAGTACCCCGACGCCG
                                                 CGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTG
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; LENGTH: 354
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3442
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US-09-738-626-3442/c
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN Ver. 3.0
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari L.
APPLICANT: Zyskind, Judith w
                                                                                                                                                                                                                                                                 Sequence 71 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                    APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA, 011A
CURRENT APPLICATION NUMBER: US 09/815,242
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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         CURRENT FILING DATE:
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o. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                            GCCTGGAATTC 224
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                                                                                                                                                  Wall, Daniel
Trawick, John D.
                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
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SENOH, AKIHIRO
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ilarity 100.0%;
Conservative (
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Pred. No. 2.1e-32;
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Sequence 6828, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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NAME/KEY: CDS
LOCATION: (1).
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NUMBER OF SEQ ID NOS: 14110
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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Local Similarity 52.8%;
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                                                                                                                                                                                                        AATTGCGTGCAGCGGTGGCAAA 1187
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Pred. No. 2.1e-29;
0; Mismatches 237;
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Best Local :
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SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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CURRENT FILING DATE: 2001-03-21
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LOCATION: (1)...(867)
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ORGANISM: Enterococcus
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
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1165 CAATTGCGT 1173
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                                                                  TTTCAAAAGGCCGAGTTTCTTTTAGAACATGGTTTTGTAGATCAGATTGTGCCAAGAAAT 807
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                                                                                                                                 ATCGGTTTTGCTGGCCGCCGTGTAATTGAACAAACGATTCGTCAAGAGTTGCCAGATGAT
                                                                                                                                                                                                                                                                             ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT 1104
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Xu, H. Howard
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53.0%;
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Pred. No. 8.3e-29;
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SEQUENCE DESCRIPTION: US-09-070-927A-458
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US-09-070-927A-458
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Patent No. US20020120116A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 458:
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APPLICATION NUMBER: 60/046,655

FILING DATE: 1997-05-16

APPLICATION NUMBER: 60/044,031

FILING DATE: 1997-05-06

APPLICATION NUMBER: 60/066,009

FILING DATE: 1997-11-14

ATTORNEY AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
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MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                 5321
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ADDRESSEE: Human Genome Sciences,
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                                                                                                                                                     5381 ATGGACGCTAATTTTATCATGGGCAGTATGGGAACGATTGTTGGTGAAAAAATCACACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
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GCCCGTATGCAAGAAGGAATTTTTTCATTGATGCAAATGGCGAAAATTTTCGGCCGCTTTG
                                   GCGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTG 924
                                                                         TTGTTTGAGCGGGCGACAGAAAAGCATTTACCAGTAGTGATTTTCACTGCATCTGGTGGT
                                                                                                               GCGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGT
                                                                                                                                                                                         TCCGATTTTTCCTTCCTCGGCGCTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 6021 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: double
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Pred. No. 3.1e-28;
0; Mismatches 230;
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; LENGTH: 870
; TYPB: DNA
; ORGANISM: Helicobacter p;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (870)
US-09-815-242-7288
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 7288
                                                                                                                  Matches
                                                                                                                                    Query Match
Best Local 9
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, APPLICANT: Ohlsen, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Identification of Essential Genes
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Similarity 50.9%;
                                   TTTACGGCCTAATGATCCTTTAAATTTCGTGGATAAAGAGAGCTATAAACAACGCATTAA
                                                                       TICTIGGAATGAAACTCCCCAATATGACAACCTCAATCAAGGCTATGCAGAGACCTTGGA 659
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Yamamoto, Robert T.
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Zyskind, Judith W.
                                                                                                                Conservative
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Pred. No. 3.3e-28;
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US-09-895-913A-97
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CURRENT APPLICATION NUMBER: US/09/895,913A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 97, Application US/09895913A Patent No. US20020160456A1
GENERAL INFORMATION:
                                                                                 Query Match
Best Local :
                                                                  Matches
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal
                                                                                                                                                                                               LENGTH: 1053
TYPE: DNA
ORGANISM: Helicobacter
                                                                                                                                                                                   FEATURE:
                                                                                 Local Similarity
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Tomb, Jean Francois
                                                                Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9854
LENGTH: 993
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Patent No. US20020061569A1
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                                                                         PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith
                                                        NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                             APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23 APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
                                                                                                             FILING DATE: 2000-12-22
                                                                                                                            FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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Zyskind, Judith W.
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FEATURE:
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LOCATION: (1)...(993)
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Local Similarity 49.6%;
les 276; Conservative
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AGCTGGCGAGCATTCT
                                                                              AGAATTTGGTGAAAACTGGTGTGATTGATGGAATTTGTGTCGCCACTCCAATTTGCGTGCAG
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                           CGGTGGCAAAAACCCT
                                                                                                                  GCCCGCGCGTTATCGAACAAACCGTTCGTGAGAAGCTCCCGCCAGGATTCCAGCGCAGTG
                                                                                                                                             GTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGG
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US-09-815-242-6133

Sequence 6133, Application US/09815242

Patent No. US2002061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karil L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

in

, 242

Essential Genes

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RESULT 14
US-09-815-242-9520
; Sequence 9520, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
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Best Local S
Matches 275
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ORGANISM: Escherichia c
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(915)
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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nes 275; Conserv
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DR APPLICATION NUMBER: 60/207,727

R FILING DATE: 2000-05-26

DR APPLICATION NUMBER: 60/242,578

DR FILING DATE: 2000-10-23

DR APPLICATION NUMBER: 60/253,625

DR FILING DATE: 2000-11-27

DR FILING DATE: 2000-11-27
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Pred. No. 9.9e-23;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PPLICATION NUMBER: 60/242,578
PRIOR PPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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APPLICANT:
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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NAME/KEY: CDS
LOCATION: (1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                     TAGGITTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTG
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                   TCCAAAAGGCAGAATTCCTATTAGAACATGGCTTTGTGGATGCTATTGTCAAAAGAAGAG
                                                                                          TTGGTTTTGCTGGGCGTCGTGATTGAAAATACGGTTCGTGAAAGCTTGCCTGAGGATT
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Zyskind, Judi
Wall, Daniel
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Judith
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49.7%;
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Pred. No. 4.4e-21;
0; Mismatches 252;
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Length Indels

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IENGTH: 654

TYPE: DNA
OGGANISM: Bacillus clausii
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(654)
OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5531
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US-09-974-300-5531
; Sequence 5531, Application US/09974300
Parent No. US20020146721A1
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PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.6%;
Best Local Similarity 51.8%;
Matches 288; Conservative
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CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
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Search completed: November 13, 2003, 06:16:26 Job time: 1310.22 secs

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SUMMARIES

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nucleotide sequences coding for the accDA gene Patent: US 6361986-A 2 26-MAR-2002;	Process for the preparation of L-amino acids by fermentation and	Tilg,Y., Eikmanns,B., Eggeling,L., Sahm,H. and Mockel,B.	1 (bases 1 to 1473)	Unclassified.	Unknown.	Unknown.		AR202320.1 GI:20256859	AR202320	Sequence 2 from patent US 6361986.	AR202320 1473 bp DNA linear PAT 20-APR-2002		

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Patent: EP 1108790-A 929 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
                                                                                                                                                                                                                                                                              Corynebacterium glutamicum
Corynebacterium glutamicum
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y Match 100.0%; Score 1473; DB 6; Length 1473; Local Similarity 100.0%; Pred. No. 6.7e-293; hes 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FT CDS (1). (1473). Location/Qualifiers 11473 . 1.1473 . /organis="Corynebacterium glutamicum" /mol_type="genomic DNA" /db_xref="taxon:1718" 275 a 414 c 456 g 328 t	27-MAY-1999 DE 19924365.4 IVENNE TILKE, LOTHAR EGGERING, BERNH VETTYNA MECKEL C12N15/09, C12N1/21, C12P13/04, C12P1 C12P13/08, C12P13/12, C12P13/20, C12P21/02//(C1 C12P13/12, C12P13/20, C12P21/02//(C1 C12R1:15), (C12P13/06, C12R1:1 C12P13/12, C12R1:15), (C12P13/20, C12R1:1 C12P13/12, C12R1:15), (C12P13/20, C12R1:1 C12P13/12, C12R1:15) (C12N15/00, C12R1:15) Key Location/Onalifier	uttle vector, and process for producing L-amino acid tent: JP 2001008693-A 2 16-JAN-2001; GUSSA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMBH Corynebacterium glutamicum JP 2001008693-A/2 16-JAN-2000 JP 2000153547	.1 GI:18632703 18693-A/2. tterium glutamicum tterium glutamicum tterium glutamicum Actinobacteria; J terineae; Coryneba s 1 to 1473) Eggering, L., Eicl le DNA, amino acid	BD004742 Replicable DNA, amino acid sequence, Corynebacterium microorganism, shuttle vector, and process for producing L-amino acid.	41 AGTCGCTTCACACGATTTGAGCGTTTAGCGCAG 1473 	.381 GGCACAATCAGCAACGCCCTCTCCGAATTGGATAACAATCCGGAGAGAGGGCGGGACGCGAC 1440 	21 AGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTC 1380	1261 GACACCAACCACGCCGCGGAAATCATAGAGGCGACAAGGCGTGCAGGCGCACGCA	01

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ALL PATENTIAL POLITION
PATENT: JP 2002191370-A 929 09-JUL-2002;

KYOWA HAKKO KOGYO CO LITD
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PN JP 2002191370-A)929

PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI 15-DEC-2000 JP 2000405096
PI SATOSHI MAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI, PI KEIKO OCHIAI,
PI KEIKO OCHIAI,
PI KEIKO OCHIAI,
PC C12N15/09, C12N15/09, C07K14/34, C07K16/12, C07K16/40, C12M1/00, PC C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12N9/02, C12P7/40, C12P13/PC 04, C12P13/08,
PC C12N1/19, C12N1/21, C12N5/102, C12N1/37, C12Q1/68, G01N33/53, PC G01N33/569, G01N33/68, G01N37/00//C12P21/08, (C12N1/21, C12R1:15), PC C12N15/00, C12N15
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Pompejus,M., Kroeger,B., Schroeder,H., Zel
corynobacterium glutamicum genes encoding
membrane synthesis and membrane transport
Patent: WO 0100805-A 25 04-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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INTSGAELSQAAEBLGIASSIARTLSKLIDAPLFVSVIIGQGVGGGALAMLPADLVY
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Peters Wendisch, P.G.
Direct Submitssion
Submitted (17-JUN-1998) F
California at Berkeley, D
Lab, 111 Koshland Hall, B
Related sequence x66112.
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Unpublished
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/strain="ATCC 13032"
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508. 1983
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/translation="MEKRPPTMVWGMEHTSALTLIDSVLDPDSFISWNETPQYDNLNQ GYAETLERARSKAKODESVITGEGTYVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIH RATELKLPLLYSPASGGARMQEDNRAFVMFUSITTAAVQRHREAHLPFLYYLRNPTMGG AMASWGSSGHLTFAREPAQIGFLGFRVVELTTGHALPDGVQQAENLVKTGVIDGIVSF LQLRAAVAKTLKVIQPVEATDRFSPTTPGVALPVMEALARSRDPQRFGLGEINETLGA DVVKLSGARAGALSPAVRVALARIGGRPVVLIGQDRRFTLGPQELRFARRGISLAREL
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/trans1_table=11
/product="putative carboxyltransferase subunit
/protein_id="CAC42827.1"
/db_xref="GI:14572582"
                                                                                                                                                                                                                     /gene="accDA"
508. .1983
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                      GGGGGCCGGCCCGTGGTGCTGATTGGGCCAGGATCGCCCGCTTCACGCTTCGGCCGCAGGAG
                                                           CTTTCTGGTGCGCGTGCTGGCGCATTGAGCCCCGGCTGTGCGCGTTGCCCTGGCGCGCATC
                                                                                                                      GACCCGCAGAGGCCTGGAATCGGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAG
                                                                                                                                     GACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAG
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LPADLVYAAENAYLSALPPEGASAILFROTNHAAEIIERGGVQAHALLSQGLIDGIVA
ETEHFVEEILGTISNALEELDNNPERAGRDSRFTRFERLAQ"
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Pred. No. 6.4
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1 (bases 1 to 2123)

1 (bases 1 to 2123)

Tilg,Y., Eikmanns,B., Eggeling,L., Sahm,H. and Mockel,B.

Process for the preparation of L-amino acids by fermenta
nucleotide sequences coding for the accDA gene
Patent: US 6361986-A 1 26-MAR-2002;
Location/Qualifiers

1. 2123

/organism="unknown"
460 a 574 c 592 g 497 t
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Sequence
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                                                              ATAGACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGAC
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61 ATAGACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGAC 120	1 GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC 60	Match 100.0%; Score 1473; DB 6; Length 2123; ocal Similarity 100.0%; Pred. No. 6.4e-293; s 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FH Key Location/Qualifiers FT gene (508). (1980). Location/Qualifiers 1. 2123 / Organism="Corynebacterium glutamicum" /mol_type="genomic DNA" /db xref="taxon:1718" 460 a 574 c 592 g 497 t	12P1: C12P1 C12N1	PD 16-JAN-2001 PF 24-MAY-2000 JP 2000153547 PR 27-MAY-1999 DE 19924365.4 PI IVENNE TILKE, LOTHAR EGGERING, BERNHARD EICKMANS, HERMANN ZAMU, PI VETTYNA MECKEL PC C12N15/09, C12N1/21, C12P13/04, C12P13/06, C12P13/06, C12P13/08, PC C12P13/08, PC C12P13/12, C12P13/20, C12P21/02//(C12N15/09, C12R1:15), (C12N1/21, PC C12P13/12, C12P13/20, C12P21/02//(C12N15/09, C12R1:15), (C12N1/21,	CH GMBH	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium. 1 (bases 1 to 2123) Tilke,I., Eggering,L., Eickmans,B., Zamu,H. and Meck,V. Replicable DNA, amino acid sequence, Corynebacterium microorganism, shuttle vector. and process for producing L-amino acid	BD004741 BD004741.1 GI:18632702 JP 2001008693-A/1. Corynebacterium glutamicum Corynebacterium glutamicum	BD004741 2123 bp DNA linear PAT 31-JAN-2002 Replicable DNA, amino acid sequence, Corynebacterium microorganism, shuttle vector, and process for producing L-amino acid.	441 AGTCGCTTCACACGATTTGAGCGCTTTAGCGCAG 1473 	381 GGCACAATCAGCAACGCCCTCTCCGAATTGGATAACAATCCGGAGAGGGGGGGACGCGAC 1440	321 AGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTC 1380	261 GACACCAACCACGCCGCGGAAATCATAGAGCGACAAGGCGTGCAGGCGCACGCA

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	gene CDS	source	COMMENT	AUTHORS TITLE JOURNAL FERENCE AUTHORS TITLE TOURNAL	RESULT 9 APO05276/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 1201 Db 1708 Qy 1261 Db 1768 Qy 1321 Db 1828 Qy 1381 Db 1888 Qy 1441 Db 1948
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Query Ma Best Loc Matches	REFERENCE TITLE JOURNAL FEATURES SOUR SOUR BASE COUNT ORIGIN	RESULT 10 AX127145/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	B 왕	A 4	д У	유 성	B 8	g 49	용성	B &	d VQ
y Match Local Similarity hes 1473; Conservat	N T E	3 20	1441 AGTCG 211724 AGTCG	1381 GGCAC 211784 GGCAC	1321 AGCCA 211844 AGCCA	1261 GACAC 211904 GACAC	1201 GCCGA 211964 GCCGA	1141 ATTGG 212024 ATTGG	1081 TCGAI 212084 TCGAI	1021 ATCAT	961 CTGCC 212204 CTGCC
100.0%; rity 100.0%; nservative	Nakagawa, S., Mizoguchi, H., Ando Yokoi, H., Tateishi, N., Senoh, A. Novel polynuclectides Patent: EP 1108790-A 7061 20-JU KYOWA HAKKO KOGYO CO., LTD. (JP Location/Qualifiers 1. 349980 /organism="Corynebacte/mol_type="genomic DNA/db_xref="taxon:1718" /note="seq 1 to long (0.600.010 0.949.980 v" 79274 a 90638 c 98727 g 81	7061 from AX114121 1 GI:140 tterium gl tterium gl tterium gl Actinoba	AGTCGCTTCACACGATTTGAGCGTTTAGCGCAG 	GGCACAATCAGCAACGCCCTCTCCGAATTGGATAACAATCCGGAGAGGGGGGGG	AGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTC	GACACCAACCACGCGGGAAATCATAGAGGGGACAAGGCGTGCAGGGGCACGCAC	GCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCCTCGGCCATCCTCTTCGGC	ATTGGTCAGGGCGTTGGCGGTGGCGCCGCCGATCTGGTCTACGCG	TGATTGCGCGCACCTTGTCCAAGCTTATCGACGCTCCCCTCCCCACCGTTTCGGTCATT	ATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGCTGAGGAGCTCGGCATCGCAAGC	CTGCGTTTTGCGCGTCGTGGCATTTCGCTGGCGCGAGCTAAACCTGCCGATCGTGTCC
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DB 6; .4e-293; s 0;	ndo,S., Hayashi,M.,A., Ikeda,M. and -JUN-2001; (JP) cterium glutamicum DNA," 8", (3.309.400) spli	980 bp DNA linear PAT EP1108790. m m Actinobacteridae; Actinomyceta bacteriaceae; Corynebacterium.	CAG 1473 CAG 211692	GATAACAATCC GATAACAATCC	GAAACCGAGCA GAAACCGAGCA	;CGACAAGGCGT ;CGACAAGGCGT	CCAGAGGGCGC	GCCATGCTGCC	GACGCTCCCC	CAGGCGGCTGA	3GCGCGCGAGCT
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	CDS		FEATURES source					COMMENT		TITLE JOURNAL REFERENCE AUTHORS	REFERENCE AUTHORS	SOURCE	ACCESSION VERSION KEYWORDS	RESULT 11 APO05217/c LOCUS DEFINITION	6 4	2	2	Db 279854	2	Db 279974
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Y., Ikeo, K., Suzuki, M. and Mashima, J. are at the Institute of Genetics, Mishima, Shizuoka, 411-8540 Japan Is at the Japan Biological Information Research Center, Tokyo, 135-0064 Japan
Tokyo, 135-0064 Japan
Tokyo, 192-0392 Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7-MAY-2002) Director-General of Biotechnology Center, titute of Technology and Evaluation, Biotechnology ihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan nite.go.jp, Tel:81-3-3481-1933, Fax:81-3-3481-8424), Y is officially affiliated with the National Advanced Industrial Science and Technology, Tsukuba, -8566 Japan
ganism="Corynebacterium efficiens YS-314"

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ki,M., Mashima,J., Itoh,T., Yamagishi,A., Nishio,Y.,
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                                                                                                                                               tion/Qualifiers
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LAGQGWGAWPACSSKLGLNSAPTPRNLNPAPAPAPAPAPAAPAEYRATVDTNTNPVVGSS
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RRGVEDPLPADDGGDY I APTPVADEWLQATLAEQLAHLMRGWWTQTYAAWLVGEADE
KNKPIHLLSPASRRDALPETRAMILGSLTRVCBEDLEADLFFHIPLAASR I PRETIRH
LLEEARWIGAVAGGGVTS PARVLTQAPAGVI PEI ADI AVAVAA PKPVDFF I VQADYTV
MVPGPLQPEWQKI IGQLADLESPGLASVYRISEASLAHAMDLGLTATEI EDFLTQHSA
TGLPQSVAYLLQDI ARRHGTLRGGPALCYLRSDDPALLHSAVEAAGALGIRQI APTVA
VSNASLIEVITALRKAGMQFVAEDALGASLDLAPRPARVPAAEQPRSAGPLDESR IRA
                                                                                         DLNTVQGIYDAVSGTLAQYGVQVPAEIQAHYNAFIGR"
                                                                                                                                                                                                       /codon_start=1
/transT_table=11
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                                                                                                                                                                                                                                                                                                                                                                                      complement(12229 ..12822)
/note="CE0894, similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                          DMEFPUPAETIGYVHPYTRINR
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GQVDALDESTGAVHRFMLHR I TEV I VD"
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complement (9548. .11851)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAC17700.1"
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DVVLLALVNTNVDETLPFRKGLAVRTINKLGYHDRKLGERVBSAVAGGRRTIBQDHW
dentity: 52 in 127
                                    'note="CE0895,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="conserved hypothetical protein"
/protein_id="BAC17703.1"
/db_xref="GI:23492731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="CE0893, similar
dentity: 50 in 62 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="CE0892, similar to AE006976-11|AAK45126.1| percent identity: 36 in 741 aa"
                                                                                                                                                                                                                                                                                                                                                           dentity: 71 in 195 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MGNMANVEKKGYVDPAWPDHDPSEGHVVTELIAPYAGASSPWGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="CE0893,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
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in 547 aa"
                           similar to AE006977-4 AAK45135.1 percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to AL583924-91 CAC31110.1 percent
                                                                                                                                                                                                                                                                                                                                                                                   AX133781-1|CAC38957.1| percent
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SdC

26058

21

81

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Query Match
Best Local Similarity
Matches 928; Conserv
 GATTGGGCAGGA---TCGCCGCTTCACGCTTGGGCCGCAGGAGCTGCGTTTTGCGCGTCG
                                       TCGCATCTCGCGGGCGACCACGGTGGCGCTGGCCCGCATCGGGGGGCCGTCCGGTCGTGCT
                                                                                                                                             CGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAGCTTTTCTGGTGCGCGTGCTGG
                                                                                                                                                                                            GAAACCACGTGGTGCGTGGGAGTCGATCATGATCACCCGGGAACCCGGTCGCCCCGGGGT
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                                                                                                                 GGCCGATCTGGTGTCGCGTCTGGGCAGAAACGTGGTGACCCTGTCCGGCACAGGTGACGG
                                                                                                                                                                                                                             CGTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTGACCCGCAGAGGCCTGGAAT
                                                                                                                                                                                                                                                                       GATCATGAGGGTTTGGGGGAGGCGTCGCCAGGCACGCCCGTGAGCTCGCCGCACCCGG
                                                                                                                                                                                                                                                                                                        AACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTTCTCCAACAACTCCTGG
                                                                                                                                                                                                                                                                                                                                             GAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAGCGGTGGCAAA
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                                                                          Conservative
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RIEfdfaagrkgfQalrvkvletprrrpQhtykpeelngiisdmvtmlegtvQpallk
GhypdrkvgeQvakilravakelea"
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Pred. No. 5.8e-114;
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Corynebacterium glutamicum
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Actinobacterium.
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X66112
                                                                                                                                                                                                        Direct Submission
Submitted (15-MAY-1992) B.
Forschungszentrum Juelich (
                                                                                                                                                                                                                                                                                    Nucleotide sequence, expression and transcriptional analysis of Corynebacterium glutamicum gltA gene encoding citrate synthase Microbiol. 140, 1817-1828 (1994)
2 (bases 1 to 3013)
                                                                                                                                                                                                                                                                       Eikmanns, B.
                                                                                                                                                                                                                                                                                                                                                                 Sahm, H.
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/mol_type="genomic_DNA"
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/t 717...>2151
838...2151
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                                               complete genome.
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AE006979.1 GI:13880475
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EILEHLGGDDLLDAIKLEEIALADDYFISRLYPNVDFYTGLIYRAMGFPTDFFTVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ORF
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1 (bases 1 to 17910)

Pleischmann, R.D., Alland, D., Bisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Salzberg, M., Land Bishai, W., Weidman, J., Khouri, H., Weidman, J., Mikula, A. and Bishai, W., Weidman, J., White, J., White, J., Weidman, J., White, J., Wh
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IAMVEVSLRDTAVIDVFGGGGRAVAGARLDAL
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/note="similar to PID:2440108; identified by sequence
similarity; putative"
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1358. .2920
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145. .1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLLSAPVDGAALNITCSGTNEQITFGLTGCRRAVPALSILTDQLAHELELLVGVSEAG
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/transl_table=11
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DGSDGAEHLVRGRFVLVGVTPAVLASILGEPVAALAPGAQVKVNMVVRRLPRLRDDSV
TPQQAFAGTFHVNETMSQLDAAYSQAASGRLPDPLPCEAYCHSLTDPSILSARLRDAG
AQTLTVFGLHTPHSVFGDTEGLAERLTAAVLASLNSVLAEPIQDVLMTDAQSKPCIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSDHDRDFDVVVVGGGHNGLVAAAYLARAGLRVRLLERLAQTGG AAVSIQAFDGVEVALSRYSYLVGLLEBRIVADLGAFVELARRFSSYTPAPATAGRSG LLIGPTGEFRAAHLAAIGAAPDAHGFAAFYRRCRLVTARLHPTLIEFLRTREQARRDI VEYGGHEAAAAQAMVDEFIGHAIAGAVANDLLRGVIATDALIGTFARMHEFSLMQNI CFLYHLVGGGTGVMHYPIGGMGSVTSALATAAARHGAEIVTGADVFALDPDGTVRYHS
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complement(4429. .6036)
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ELSTIRLLAKLPTIAAYAYKSVGQPFLYFDNSJTLVENFELLTGGFPAEFYQADDEV
VRALDMLFILHADHEQUKSTSTYRLVGSSRAHLFTSISGGINALWGFHAGGANQAVLB
MLEGIRDSGDDVSEFVRKVKNREAGVKLMGFGHRVYKNYDPRARIVKEQADKILAKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MT0922"
6433. .7413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="MT0921.1"
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/gene="MT0921.1"
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GGAVSGIGGHNAAMAVLACLASRRKSP"
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PGWIAHWREMHDEGDSKIGRPRQIYTGYTERDYVTIDAR"
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FDVGFANTAAAKSSITYIDGDAGILRYRGYPIDQLAEKSTFIEVCYLLIYGELPDTDQ
                                                                                                                                                                                                                           /gene="MT0923"
7426. .7578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="oxidoreductase, putative"
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/db_xref="GI:13880479"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="MT0922"
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/transl_table=
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/db_xref="GI:13880478"
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                           translation="MDFVIQWSCYLLAFLGGSAVAWVVVTLSIKRASRDEGAAEAPSA
                                                                                                                                                                           note="identified
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TGCAGGAAGACCAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTC 424
                                                                           AGCGGGCGÁCCGCCGAGCGGCTGCCGCTACTGGCGTCACCAAGCTCGGGAGGCACCCGGA 11471
                                                                                                                           ACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCGCGCA 364
                                                                                                                                                                             TCGACTTCCTGGGCGGCTCGATTGGGGTGGCAGCGGCCGAACGGATCACCGCCGCCGTCG 11531
                                                                                                                                                                                                                           TITCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTC 304
                                                                                                                                                                                                                                                                             CGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATT
                                                                                                                                                                                                                                                                                                                                                                           TAGCCGÁCTCCTÁTGCGCGGGAGCTGGCCGCCGCTCGGGCGGCGCCACGGACGAAT 11651
                                                                                                                                                                                                                                                                                                                                                                                                                     TCAATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGCCAAGGCCAAATGCGATGAAT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG 11711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /producc="sensor histidine kinase"
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EVHGASEAIE1ALBDDGREWLMDUNGTGSRIEBTLSALERLAGELSTSDDHYPDITTDLLD
EXAAHDAARIYPDLDVSLVPSPTCIIVGLPAGLRLAVDNAIANAVKHGGATLVQLSAVS
SRAGUEIAIDDNGSGVPEGERQVVFERFSRGSTASHSGSGLGLALVAQQAQLHGGTAS
TENEDICCAETUTELOSE"
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complement (8122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GP:2440114; similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (9473. .10183)
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kskpptarkpavksgtkreesptaktkvatesaaeqipvagepaaepipvagepaari
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7575. .8105
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/db_xref="GI:13880485"
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/note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MGGMDTGVTSPRVLVVDDDSDVLASLERGLRLSGFEVATAVDGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MT0926"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="MT0925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="MT0926"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="similar to PID:2440113; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 312.6; DB 1
Pred. No. 3.7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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1.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulator"
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21;

244

gene

CDS

RESULT 14 MTCY31/c	QY 1307 CGCACGCACTTTTAAGCCAAAGGGCTTATCGACGGATCGTCGCCGAAAACCGAGCACTTTG 1366	OY 1187 ATCTGGTCTACGCGGCCGAAAACGCCTGGCTGTCCCACCAGAGGGGCGCCTCGG 1246		AAAGGGCAGTAGGCGGCGGGGGAAGCACTG GTGGCATTTCGCTGGCGGCGCGAGCTAAACC	The contract of the control of the c	11290 TTCTGGGACCACGGGTCTAAAAACTGGTTGCATTGAGCGTCCCATCCGAACGGTTCCAAAACGGTTGCTCTAATTGAGCGACCCCTTCCCATCCGGCGTCCAAAACGGTGTGAAAACTGGTTGATTGA	11470 TGCAAGAAGGCACGGTCGCGTTTCTGCAGATGGTGAAAGATCGCTGCGGCCATCCAGCTGC 425 ACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTTGCGCAATCCCACGATGGGTGGCGCCA
/product="hypothetical protein kv08/4c" /protein_id="CAA97403.1" /db_xref="GI:1314011"	/note="Rv0874c, (MTCY31.02c), len: 386. Unknown, very similar to Mycobacterium tuberculosis MTCY20H10 9 (383 aa, E():0, 81.5% identity in 383 aa overlap) and to hypothetical proteins from SPU62616 1 Synechococcus sp. (280 aa; E(): 6.3e-26; 35.2% identity in 264 aa overlap) and SYCSLILH 102 Synechocystis sp (447 aa; E(): 1.1e-18; 29.5% identity in 400aa overlap)" /codon_start=1 /ransT_table=11	/mol_type="genomic DNA" /strain="H37Rv" /db_xref="raxon:8332" /clone="Y31" gene complement(541214) /gene="Rv0874c" CDS complement(541214)	initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. FEATURES Source Jorganism="Mycobacterium tuberculosis H37Rv"	Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CANTTON: In some cases we may not have predicted the correct	MEDLINE 98295987 MEDLINE 98295987 PUBMED 9634230 REFERENCE 2 (bases 1 to 37630) AUTHORS Parkhill, J. TITLE Direct Submission Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:1314009.	AUTHORS Cole,S.T., Barosch,R., Parkhill,J., Garnier,T., Churcher,C., Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry III,C.E., Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T., Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S., Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J., Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A., Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S., Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and Barrell,B.G. Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence	ISM S S ON

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M. tuberculosis sequencing at the Sanger Centre are the World Wide Web.

//www.sanger.ac.uk/projects/M_tuberculosis/) CDS have ered from the original cosmid submissions but the old ations are in brackets after the new gene numbers. tion was based on a Hidden Markov Model of TB genes in TBparse (Krogh) supplemented with visual inspection al base preference in codons, especially where there is in the observed/expected third position G + C. n some cases we may not have predicted the correct codon. Where possible we choose an initiation codon or ttg) which is preceded by an upstream ribosome e sequence (optimally 5-13bp before the initiation this cannot be identified we choose the most upstream
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don,S.V., Eiglmeier,K., Gas,S., Barry III,C.E.,
lcock,K., Basham,D., Brown,D., Chillingworth,T.,
ries,R., Devlin,K., Feltwell,T., Gentles,S.,
royd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
hy,L., Oliver,S., Osborne,J., Quail,M.A.,
hy,L., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
lares,R., Sulston,J.E., Taylor,K., Whitehead,S. and
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37630)
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tuberculosis H37Rv
nobacteria; Actinobacteridae; Actinomycetales;
eae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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tuberculosis H37Rv complete genome; segment 41/162.
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on/Qualifiers
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gene

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GDYLGVSYEDGNAATHRFIAHLPGYQGWQWAVVVASYSGADHATISEVVLVPGPTALL
APDWVPWEQRVRPGDLSPGDLLAPAKDDPRLVPGYTASGDAQVDETAAEIGLGRRWVM
                                                                                                                                                                                                                                                                                                                                                                    /note="Rv0877, (MTCY31.05), len: 262, unknown,
equivalentto MLCB57_13 Mycobacterium leprae cosmid B57
033058 HYPOTHETICAL 28.2 KD PROTEIN (269 aa; E(): 0;80.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGPALDRLQHGRRVALALSFGLRTALAVVLIMNYDGATGSFPSWVLYPCALAMMVFS
KSFSVLRSAVTPRVMFPTIDLVRVNSELTVFGLLGGTLAGGALRARVEFEVEVLLGGLF
GALFVVVAITIAGASLSRRTIPRWFEVTSGEVPATLSYHEDRGELRRRWFEEVKNLGGTL
LRQPLGRNIITSLWGNCTIKVNVGFLFLYPAFVAKAHEANGWVQLGMLGLIGAAAAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein Rv0876c"
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/db_xref="SI:1314013"
/db_xref="SIISS-PROT:Q10564"
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YLPPLGEQPEPERSRVPPRTTRAGERITVTRADAMRSREMGSRMYLLVHRAATADGAD
KSGLTALTWPYMANFAVDSAMAVALANTLFFAAASGESKSRVALYLLITIAPFAVIAP
KSGLTALTWPYMANFAVDSAMAVALANTLFFAAASGESKSRVALYLLITIAPFAVIAP
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/translation="MKRGVATLPVILVILLSVVAGAGAWLLVRGHGPQQPEISAYSHG/translation="MKRGVATLPVILVILLSVVAGAGAWLLVRGHGPQQPEISAYSHGHLTRYGPYLVGUVVLLDDCQTPGAGGELPVSERYPVQLSVPEVISRAPWRLLQVYQDAWTTSTLFRPDTRLAVTIPTVDPQRGRLTGIVVQLLTLVVDHSGELRDVPHAEWSVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Rv0875c, (MTCY31.03c), len: 162, unknown, possibly exported protein, highly similar toMLCB57 II Mycobacterium leprae cosmid B57, 033056 HYPOTHETICAL 18.1 KD PROTEIN (162aa). FASTA scores: opt: 789 z-score: 963.4 E(): 0; 71.4%identity in 161 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRTGSGALITGYRFDRTARDLHLLLPDPYTFPSNLLIBHPNTDLPGTAVVGGVVSGGR
RRGDTRLFRDHPVLTSGVVGVRLPGMRGVPVVSGCREPIGYPYLVTGADGILITELGG
RPPLQRLREIVEGLSPDERALVSHGLQIGIVVDEHLAAPGQGDFVIRGLLGADFSTGS
IEIDEVVQVGATMQFQVRDAAGADKDLKUTVERAAARLFGRAAGALLFTCNGRGRMF
GVADHDASTIBELLGGIPLAGFFAAGEIGPIAGRNALHGFTASMALFVDDME"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Rv0877"
3583. .4371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFAGNFTSARLQLGRPAVLVVRCTVLVTVLAIAAAVAGSLAATAIATLITAGSSAIAK
ASLDASLQHDLPEESRASGFGRSESTLQLAWVLGGAVGVLVYTELWVGFTAVSALLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Rv0876c, (MTCY31.04c), len: 548; unknown; possible membrane protein, highly similar to MLCB57 12 Mycobacteriumleprae cosmid B57 033057 HYPOTHETICAL 61.7 KD Mycobacteriumleprae cosmid B57 033057 HYPOTHETICAL 61.7 KD PROTEIN (579aa). FASTA scores: opt: 2850 z-score: 2863.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Rv0875c"
                                                                                                           /transT_table=11
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/db_xref="SWISS-PROT:Q10539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="gagg,
3583. .4371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (3457. .3465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLAQTIVSFRGDSLIPGLGGNRPVMAEQETTRRGAAVAPQ"
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/trans1_table=11
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/db_xref="GI:1314012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (1314. .1802)
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TDRAADVLSAVLQMIDPPALVGCIAQAIVAGRHEIEDEPAVVVWLASGLAAETFQLDF
                                                                                                                                                                                                                                                                                                                              identity in 257aa overlap.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="Rv0877"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="gaggtgatc, potential rbs upstream of Rv0876c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl
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                             245
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
TTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCCGCGTCCGGTGCGCATCATGAAGGCGATTC 304
                                                                                  CGGTGCAGACCGGTGAGGGACGCGTATTCGGGCCGGGGGGGCCGTGGTCGCCTGTGAGT
                                                                                                                                 CGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATT
                                                                                                                                                                                   TAGCCGACTCCTATGCGCGGGAGCTGGGCCGCCTCGGGCGGCCACCGGCGCGGACGAAT
                                                                                                                                                                                                                                      TCAATCAAGGCTATGCAGAGACCTTGGAGCGGCTCGAAGCAAGGCCAAATGCGATGAAT 184
                                                                                                                                                                                                                                                                                        ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG
                                                                                                                                                                                                                                                                                                                                     ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC 124
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /HOUGE="RV0880, (MTCY31.08), len: 143, unknown, equivalent to MLCB57_15 Mycobacterium leprae cosmid B57 (143 aa)
033060 HYPOTHETICAL 15.8 KD PROTEIN. FASTA scores: opt:
818 z-score: 980.3 E(): 0; 89.5% identity in 143 aa
overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="gga (or aagg) potential rbs upstream of Rv0878c"
complement(5989. .6264)
/gene="Rv0879c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA97385.1"
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/db_xref="GI:1314016"
/db_xref="SI:1314016"
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AGFLNIGSGNTGDYNFGIGNIGNANLGWGNIGNANLGSGNAGFENFGNGNDGNTNFGGGN
AGFLNIGSGNEGSGNIGFGNAGDDNTGWGNSGDTNTGGFNSGDLNTGIGSPTTQGVAN
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/note="Rv0879c, (MTCY31.07c), len: 91 unknown, equivalent /note="Rv0879c, (MTCY31.07c), len: 91 unknown, equivalent to MLCB57 14 Mycobacterium leprae 033059 HYPOTHETICAL 9.8 KD PROTEIN (91 aa), E(): 1.2e-25, 76.9% identity in 91 aa
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/gene="PPE"
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/translation="MSVENSQIREPPPLPPVLLEVWPVIAVGALAWLVAAVAAFVVPG
LASWRPVTVAGLATGLLGTTIFVWQLAAARRGARGAQAGLETYLDPK"
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/product="hypothetical protein
/protein_id="CAA97386.1"
/db_xref="GI:1314017"
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Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire

Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire

Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex

15, France. e-mail:tgarnier@pasteur.fr Submitted on behalf of the

Mycobacterium bovis sequencing teams, TB Research Group, Veterinary

Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlestone,

Surrey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus,

Hinxton, Cambridge CB10 15A, UK. PT4 Annotation, Genopole, Institut

Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France.

Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28

rue du Docteur Roux, 75724 Paris Cedex 15, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete genome sequence of Mycobacterium Online Publication PNAS 10.1073/pnas.1130426100 ( Microbiology )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garnier,T., Eiglmeier,K., Camus,J.-C., Medina,N., Mansoor,H., Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon, Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L., Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V.
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Mycobacterium bovis subsp. bovis AF2122/97
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Mycobacterium bovis subsp.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compiete genome.
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                                                            ENRTPVANPQQVSVPEGGTVGPVRFDACDPDGNRMTFAVRERGAPGGPQHGIVTVDQR
TASFI YTADDGFVGTDTFSVNVSDDYSLHVHGLAGYLGPFHGHDDVATVTVFVCNTPT
DTISGDFSMLTVNIAGLBFPLSSAILPRFFYKEIGKRLNAYVVANVQEDFAYHQFLI
KKSKMPSQTPPEPFTLMPIGVPFSDGLNTLSEFKVQRLDRQTWYECTSDNCLTLKGF
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SDDQSALLQFAQVNGLTDAWVQVEHGPTTPPFAPTCMVGNECELLDKIFYRSGQGVTL
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VDACSPLGGSASSLAAIPGASVPQVGVRQVDPGSIPDDLLNALIDPLAAVRNGLVPII
                                                                                                                                                                                                                                                                                                                                                 490 aa, from Mycobacterium tuberculosis strain H37Rv, (100,0% identity in 490 aa overlap). Probable exported protein. Equivalent to AAA45157.1 from Mycobacterium tuberculosis strain CDC1551 (507 aa) but shorter 17 aa. Contains possible N-terminal signal sequence."
                  complement
                                       QAVSYGNEAPKFFNSKGEPLSDHSPAVVGFHYVADNVAVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mycobacterium
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="Mb0912"
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                                                                                                                                                                                                                                                                                                         codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="taxon:233413"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   locus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tag="Mb0912"
                                                                                                                                                                                                                                                                                                           table=11
                  (2205. .3326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  len: 490 aa. Equivalent to Rv0888,
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bovis AF2122/97 complete
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Bivod

len:

CDS

SdC

gene

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/notes_mb0914c, ., len: 882 aa. Equivalent to Rv0890c, /notes_mb0914c, ., len: 882 aa. Equivalent to Rv0890c, len: 882 aa, from Mycobacterium tuberculosis strain H37Rv, (99.9% identity in 882 aa overlap). Probable transcriptional regulatory protein, LuxR family, highly similar (but shorter 238 aa in N-terminus) to NP 302202.1|NC 002677 possible transcriptional regulator from Mycobacterium leptrae (1106 aa). Also highly similar (generally in part) to others e.g. T50568 probable multi-domain regulatory protein from Streptomyces coelicolor (1334 aa); p10957|NARL ECOLI nitrate/nitrite response regulatory protein from Escherichia coli (216 aa), FASTA scores: opt: 193, E(): 6e-06, (37.4% identity in 99 aa overlap); etc. Also highly similar to others from Mycobacterium tuberculosis e.g. MTCY02B10_22, MTV008 44, MTV036_21, and MTCY31_24. Contains p80017 ATP/GTP-binding site motif A (P-loop), P800622 Bacterial regulatory proteins, luxR family signature, and probable helix-turn helix motif from aa 836 to 857 (Score 1559, +4.50 SD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (100.0% identity in 373 aa overlap). Probable cith (alternate gene name: glth), citrate synthase 2 (EC 4.1.3.7), highly similar to others e.g.

CAB95899.1 | AL359988 putative citrate synthase from Streptomyces coelicolor (387 aa); p39119 (ISY BACSU citrate synthase II from Bacillus subtilis (356 aa), FAST7 scores: opt: 586, E(): 5.8e-30, (33.8% identity in 367 aa overlap); etc. Also similar to Rv0896 [MTCY31.24 from Mycobacterium tuberculosis (29.2% identity in 274 aa overlap) and Rv1131. Contains PS00480 Citrate synthase signature. BELONGS TO THE CITRATE SYNTHASE FAMILY."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILEDQRFHRLAVSTAVRARALADKAMLSTWLATSPVGATDIIAPAQQALAMAREVGDP
AALVRALTACGCSSGYVAAEAAAPYFAEATDLARAIDDKWTLCQIIYWRGYGTCISGDP
NALRAAAEECRDLADTIGDRFVSRHCSLWLSLAQMWAGULTEALELSREITABEAESR
DVPTKVLGLYTQAQVLAYCGASAAHAIAGACIAAATELGGVYQGIGYAAMTYAALAAG
                                                                                                                                                                                                                                                         LRAS I DWSHALLTETEQ I LFRR LAPFVGGFDLAAVRAVAAGSDLDPFSVLDQLTLLVD
KSLVVADDCQGRTRYR LLETVRRYALEKLGDSGEADVHARHRDYYTALAAS LNTPADN
DHQRLVARAETE I DNLRAAFAWSRENGH I TEALQLAS SLQP I WFGRAHLREGLSWFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="mrallaqnrlvtlcgtggygktrlaiqiasaselrdglcfydla
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complement(3413. .60)
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HILEQKRLGKLVRPSAIYVGPGPRSPESVDGWERVLTTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAAAVGEI CRRLDGI PLAI EFAAARVRSMS PLEI ADGLDDC FRLLAGGVRGAVQRQQT
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complement(2205. .3326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN PROBABLY LUXR-FAMILY)"
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S 밁 S

125

TCAATCAAGGCTATGCAGAGACCTTGGAGCGGCTCGAAGCAAGGCCAAATGCGATGAAT 184 ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG 21555 ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC 124 Matches Best Query Match

Local Similarity 54.1 nes 717; Conservative

21.2%;

Score 312.6; I Pred. No. 2.6e 0; Mismatches

2.6e-54; DB 1;

Indels

Gaps

w ••

Length 327650;

0

gene

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/note="Mo0916, -, len: 495 aa. Equivalent to Rv0892, len: /note="Mo0916, -, len: 495 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 495 aa overlap). Probable monoxygenase (EC 1.14.-.), highly similar to others e.g. NP 250787.1 | NC 002516 probable flavin-binding monoxygenase from Pseudomonas aeruginosa (491 aa); CAB59668.1 | AL132674 monooxygenase from Streptomyces coelicotor (519 aa); p12015 | CYMO ACIS cyclohexanone monoxygenase from Acinetobacter sp. (542 aa), FASTA scores: opt: 489, E(): 6.8e-26, (30.3% identity in 492 aa overlap); etc. Also highly similar to Rv0565c, Rv3854c, Rv383, etc from Mycobacterium tuberculosis. Has hydrophobic stretch at N-terminus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus tag="Mb0915c"
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/note="Mb0915c, ., len: 285 aa. Equivalent to Rv0891c,
len: 285 aa, from Mycobacterium tuberculosis strain H37Rv,
len: 285 aa, from Mycobacterium tuberculosis strain H37Rv,
len: 285 aa overlap). Possible
transcriptional regulator, highly similar in N-terminus to
Ng 302202.1 NC 002677 possible transcriptional regulator
from Mycobacterium leprae (1106 aa). Also highly similar
to several Mycobacterium tuberculosis putative
transcriptional regulators e.g. Q1102 MTCY02B10 22
PROBBELE TRANSCRIPTIONAL REGULATORY PROTEIN (1159 aa),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mlfnavhnslppnididhailrgedhpptcakcvargrisalgs
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grlpadawlvdlgrhplrglprpewvmolchpdirekfpplktakssptsilpagftt
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EAIAYAQRGRGERKRPARGWGSLTPTERDVVRLVSEGLSNKDIAKRLFVSPRTVQTHL
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GFDSHAFFRPMQLTGRDGIRIDDVWQDGPHAHQTVAIPGFPNFFMMLGPHSPVGNFPL
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TAVAESQAEHIVQWIKRWRHGEFDTMEPKSAATEAYNTVLRAAMPNTVWTTGCDSWYI
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3 1246 1 3 20418	1187 ATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCTCGG	
3 1186 3 20478	1127 CCGTTTCGGTCATTATTGGTCAGGGCGTTGGCGGTGGGCGCTGGCCATGCTGCCGCCG	
1126 1 20538	1067 TCGGCATCGCAAGCTCGATTGCGCGCACCTTGTCCAAGCTTATCGACGCTCCCCCCA	
2 1066 3 20598	1007 TGCCGATCGTGTCCATCAACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGC	
1006 20658	947 TIGGGCCGCAGGAGCTGCGTTTTTGCGCTGGCATTTTCGCTGGCGCGCGC	
C 946 3 20718	902 GGGGCCGGCGGTGGTGCTGATTGGGCAG	
3 901 3 20778	842 TTTCTGGTGCGCGTGCTGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCTGGCGCGCATCG	
C 841 T 20835	782 ACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAGC	
3,781 C 20895	725 CTCCAACAACTCCTGGGGGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTG	
T 724 C 20955	665 GIGCAGCGGTGGCAAAAACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTT	
C 664 C 21015	605 AGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATGGAGTTGTTGTCGCCACTCCAATTGC	
C 604 A 21075	545 TCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGC	
T 544 21135	485 TGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGGCGCAGATAGGTT	
A 484 T 21195	425 ACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCA	
C 424 C 21255	365 TGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTC	
A 364 21315	305 ACCGCGCCACAGAGCTGAAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGGCGCA	
C 304 G 21375	245 TTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGGTCGGTGCGCATCATGAAGGCGATTC	
T 244 21435	185 CGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATT-	
T 21495	21554 TAGCCGACTCCTATGCGCGGGAGCTGGCCGCCGCTCGGGCGGCCACCGGCGGCGACGAAT	

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Дb	γQ	DЬ	Qy	Db	Qy
20297 CAGACGA 20291	1367 TTGAAGA 1373	20357 CGGCCGACCTACTGAAGTCGGGGATTGTCGACACCATCGTGCCGGAGTACCCCGGACGCCG 20298	1307 CGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAAACCGAGCACTTTG 1366	20417 CGATCGTGTTCCGAGACACTGCTCATGCCGCCGAACTCGCTGCCGCCCAAGGCATCCGGT 20358	1247 CCATCCTCTTCCGCGACACCAACCACGCCGCGGAAATCATAGAGCCGACAAGGCGTGCAGG 1306

Search completed: November 13, 2003, 00:10:39 Job time: 5538.03 secs

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Result
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Maximum Match 10
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Maximum DB
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             312.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
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AAI99683
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AAC82733
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  C glutamicum codin
C. glutamicum accD
Corynebacterium gl
C. glutamicum accD
C glutamicum codin
Mycobacterium tube
Mycobacterium tube
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Magnetospirullum s Genomic fragment #	Listeria monocytog	Genomic sequence o	DNA sequence upstr	Haemophilus influe	2CFE 67 coding seq	Streptococcus pneu	Listeria innocua D	Listeria innocua c	Streptococcus poly	Streptococcus poly	Streptococcus pneu	Haemophilus influe	Streptococcus pneu	S. pneumoniae deri	Haemophilus influe	CFE 67 coding sequ	S. pneumoniae type	Bacillus clausii g	Streptococcus pneu	DNA encoding novel	DNA encoding novel	E. coli DNA for ce	Salmonella typhi D	Human R1128 gene c	N. meningitidis B	Neisseria meningit	H. pylori GHPO 451	Helicobacter pylor					erococcus	N. gonorrhoeae nuc	Pseudomonas aerugi

ALIGNMENTS

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RESULT 1
AAH65894
ID AAH6
XX AAH6
XX AAH6
XX AAH6
XX COry
KW Cory
KW Orga
XX Cory
KW Orga
XX Cory
XX EP11
PD 20-J
PN EP1-F
PN EP1-F
PN 18-F
PR 10-A
PR 00-A
PR 00-A
PR 00-A
PR 00-A
PR 00-A
PR 01-A
PR
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07-APR-2000;
03-AUG-2000;
WPI; 2001-376931/40
                                                                                Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum.
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                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glutamicum coding sequence fragment SEQ ID NO: 929.
                                                                            Mizoguchi H,
Senoh A, Ik
                                                                                                                                                                                                                                                                                              99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                                H, Ando S, Hayashi M, Ikeda M, Ozaki A;
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SXCCCCCCCCCCCXSXTTTTXXX

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Query Match
Best Local :
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1473 BP; 275 A; 414 C; 456 G; 328
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                                      CAGCAGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAA
                                                                                                       GGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTG
                                                                                                                                                                                       GCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATA
                                                                                                                                                                                                                                                 CGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGC
                                                                                                                                                                                                                                                                       CGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGC
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Query Match
Best Local Similarity
Matches 1473; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1), replicable in coryneform microorganisms coding for an accDA gene, a fully defined 491 as sequence; (2) coryneform microorganisms the shuttle vector pzlaccDA contained in Corynebacterium glutamicum DSM 12785; and (4) a process for producing L-amino acids, comprising culturing a coryneform bacterium that overexpresses the accDA gene. Coryneform bacterium that overexpresses the accDA gene. Coryneform bacteria transformed with (1) so that they overexpress the accDA gene useful in animal feeds, in human medicine and in the pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 12-15; 20pp;
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                                                                                           Corynebacterium glutamicum nucleic acids encoding membrane con and membrane transport proteins or their portions, useful for identifying C. glutamicum or related bacteria, and as markers transformation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation; genome mapping; genetic engineering; ds.
AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine
                                                                                                                                                              WPI; 2001-071486/08.
P-PSDB; AAB76522.
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979 900 919 840 859 chemicals, for modulating fine chemical production in C. glutamicum related bacteria (e.g. Brevibacterium lattofermentum), the typing or identification of C. glutamicum or related bacteria, as reference por for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in a in C. 5 'n 8 an

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transformed coryneform bacteria producing increased yields of transformed coryneform bacteria producing increased yields of transcribes, especially L-lysine - claim 1; page 9-11; 20pp; German. claim 1; page 9-11; 20pp; German. critically in coryneform microorynebacterium glutamicum DNA rhis invention describes a novel cloned corynebacterium glutamisms (cli), replicable in coryneform microoryneisms of the invention also describes (1) a polypeptide derived ganisms (cli), replicable in coryneform microoryneisms (1), replicable in coryneform microoryneisms of transformed with one or more copies of (1); (3) the shuttle and a fully defined and in corynebacterium glutamicum psh 1278; and a fully defined one or more copies of (1); (3) the shuttle and cransformed with (1) so that the accDA gene. Coryneform producing L-amino acids, comprising culturing a coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seterium that (1) so that they overexpress the accDA gene are coryneform seteri	- 1
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DT 26-SEP-2001 (first entry)
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C Gryneform bacterium; amino acid
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07-APR-2000;
03-AUG-2000;
                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and from coryneform bacterium, measuring expression amount and from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                Sequence
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12-NOV-1999;
12-NOV-1999;
01-FEB-2000;
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P-PSDB; /
Disclosure; Page 74; 207pp; English
                                                    Identifying nucleotide or polypeptide sequence for use as drug target
involves providing algorithm that analyzes a functional relationship
between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                   Eisenberg
                                                                                                                                                                                                                                                                                                                                13-NOV-2000;
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DB; AAG81130.
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This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polypucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of

Sequence 1488 BP; 220 A; 509 C; 524 G; 235 T; 0 other;

21.2%;

DB 22;

Length

Best Local Similarity Matches 717; Conserv 365 212 245 152 125 92 32 65 TGCAGGAAGACGATCGAGCTTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTC TCAATCAAGGCTATGCAGAGACCTTGGAGCGGCTCGAAGCAAGGCCAAATGCGATGAAT AGCGGGCGACCGCCGAGCGGCTGCCGCTACTGGCGTCACCAAGCTCGGGAGGCACCCGCA TCGACTTCCTGGGCGGCTCGATTGGGGTGGCAGCGGCCGAACGGATCACCGCCGCCGTCG rrrccrrccrceeceerrcrrreeecaceercecerceerececarcarcareaaeecearrc CGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATT TAGCCGACTCCTATGCGCGGAGCTGGCCGCCGCCTCGGGCGCCACCGGCGCGACGAAT ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC Conservative <u>.</u> Score 312.6; DB 2 Pred. No. 1.5e-78; 0; Mismatches 589 589; Indels 21; Gaps 184 124 424 331 364 271 304 244 151 91 211 w

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37RV (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -
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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1. H37Rv (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic

BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

S 밁 Ś 밁 S 밁 Ş Matches Query Match 1008027 1008087 1008147 Local Similarity les 717; Conserv 185 65 TTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTC 304 CGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATT ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG 1008088 TCAATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGCAAGGCCAAATGCGATGAAT 184 ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC 124 Conservative 21.2%; 0, Score 312.6; DB 22; Length 4411529; Pred. No. 5.4e-77; 0; Mismatches 589; Indels 21; Ga Gaps 244 1007968

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                                                                                                                                             genes, their use in the discovery of novel antibiotics, the essential CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC gneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen CC for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                    Sequence 873 BP; 152 A; 285 C; 276 G; 160 T; 0 other;
                                                                                                                  of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Seq ID No 7800; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611495/70.
P-PSDB; AAU36304.
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
23-OCT-2000;
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23-MAY-2000;
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                                                                                                  ftp.wipo.int/pub/published_pct_sequences
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2000US-253625P.
2000US-257931P.
2001US-269308P.
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2000US-206848P.
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Score 122.8; DB 23;
Pred. No. 1.5e-24;
Wismatches 237;
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The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins a antibodies that specifically bind to the proteins. The composition
                                        Disclosure; Page 377; 815pp; English.
                                                            New protein
medicament f
                                                                                                                                                            12-FEB-2001; 2001GB-0003424
                                                                                                                                                                                                    10-OCT-2002
                                                                                                                                                                                                                      WO200279243-A2
                                                                                                                                                                                                                                        Neisseria gonorrhoeae
                                                                                                                                                                                                                                                             Antibacterial;
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)B; ABP78030.
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                                                                                                                     Pizza M,
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Best Local Similarity
Matches 280; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising the protein, nucleic acid or antibody is useful for t manufacture of a medicament for treating or preventing N. gonorr infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic a molecules of the invention.
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    TTG
                                                          CAGCAGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAA
                                                                                                                                                                                   GCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCGCAGATA
                                CAACGCGCCGAGTTTCTGCTGGAAAAAAGGCGCGATCGACCAGATTGTCGACCGCCGAT
                                                                                            GGTTTTGCCGGTCCGCGCGTGATTGAGCAGACGGTGCCGCAAACGCTGCCGGAAGGCTTC
                                                                                                                          GGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTG
                                                                                                                                                         GTATCTGCCAGCTTCGCATTTTTAGGCGATGTCGTGCTTGCCGAACCGAACGCGCTGATC
                                                                                                                                                                                                                       TIGCIGACGGAAAAACGCCIGCCGTTTATATCGGTGTTGACCGATCCGACTATGGGCGGC
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nilarity 51.6%;
Conservative
   663
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Pred. No. 2.2e-24;
0; Mismatches 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263;
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RESULT 11
AAS53191
ID AAS53
XX AS53
XX AS53
XX ANS53
XX ANTis
DT .13-FE
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KW Antis
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ATG

13-FEB-2002 AAS53191; (first entry)

Enterococcus faecalis DNA for cellular proliferation protein #619.

Antisense; ds; prokaryotic cellular proliferation antibiotic; antibacterial; drug design. drug design gene;

Enterococcus faecalis

WO200170955-A2

27-SEP-2001

21-MAR-2001; 2001WO-US09180.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC a wide variety of organisms. The present sequence encodes an CC a wide variety of organisms. The present sequence encodes an CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 259
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23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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Yamamoto RT,
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16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT
                                                          GGTGTTACCGCAAGTTTTGCGATGGATGGCGATATTATTTTGGCAGAGCCTCAGAGTTTA
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                                                                                                                                                                               CAACGGCATAACAAAGCAGGCTTGCTGTATCTTACGGTATTGACTGATCCAACGACTGGC
                                                                                                                                                                                                                                      CAGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCCGCAATCCCCACGATGGGT
                                                                                                                                                                                                                                                                                                 GCCCGTATGCAAGAAGGAATTTTTTCATTGATGCAAATGGCGAAAATTTCGGCCGCTTTG
                                                                                                                                                                                                                                                                                                                                                        GCGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                  TTGTTTGAGCGGCGACAGAAAAGCATTTACCAGTAGTGATTTTCACTGCATCTGGTGGT
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2000US-206848P
2000US-207727P
2000US-242578P
2000US-253625P
2000US-257931P
2000US-257931P
2001US-269308P
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Xu HH;
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Pred. No. 4.7e-24;
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178 GATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTG 237

Query Match Best Local S Matches 259

Similarity

8.2%;

259;

Conservative

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Score 121; DB 20; Pred. No. 1.1e-23; 0; Mismatches 230;

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RESULT 12
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06-MAY-1997;
16-MAY-1997;
                                                                                                         A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12338 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in a animal and monitoring
                                      progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                    New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fouse in vaccines for prevention or attenuation of Enterococcus
 Sequence
                                                                                                                                                                                                                                             Claim 1; Page 1691-1694; 2084pp; English
                                                                                                                                                                                                                                                                                                                                                                          Barash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        attenuation;
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97US-0044031.
97US-0046655.
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G; 1673 T; 6 other;
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RESULT 13
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                                                                                                                      (KUNS/)
          Computer readable medium having recorded nucleotide sequence useful for detecting Enterococcus infections in animals -
                                                                                                                                                           04-MAY-1998;
                                                                                                                                                                                 04-MAY-1998;
                                                                                                                                                                                                            29-AUG-2002
                                                                                                                                                                                                                                  US2002120116-A1
                                                                                                                                                                                                                                                          Enterococcus faecalis.
                                                                                                                                                                                                                                                                                         Computer readable medium; Enterococcus faecalis; microbe; growth; pathogenicity; vaccine; resistance; Enterococcal infection; commercial; therapeutic; industrial; fermenting; sugar source; metabolite; vaccine; biochip technology; antibacterial; modulator of nucleic acid expression
                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis contig sequence #458.
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                                                                                                        KUNSCH C.
DILLON P.
BARASH S.
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                                                                                 Dillon
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KW SID;

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ABX65750

standard; DNA; 676

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Helicobacter

pylori selected interacting domain (SID)

Protein-protein interaction; ulcer; selected SID; gene; ds.

interacting

DNA #349. ing domain;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention is userui to diagnose the presence of E.faecalis in a sample or determining the presence of the presence of E.faecalis in a sample. The invention is also useful for modulating the growth or pathogenicity of E.faecalis, in a vaccine to confer resistance to Enterococcal infection, for commercial, therapeutic and industrial purposes, and for fermenting a particular sugar source or to produce a particular metabolite. The invention is useful for detecting diseases related to Enterococcus infections in animals, and for detecting E.faecalis using biochip technology. The present nucleic acid sequence represents an Enterococcus faecalis contiguation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animals, and for detecting E.faecalis using biochip technology. The present nucleic acid sequence represents an Enterococcus faecalis con DNA sequence of the invention.

Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at http.sequdata.uspto.gov.
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CTTTTGCGT
                                                                                                                                                                                                                                        GGCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCGCAG
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                                   CAATTGCGT
                                                                  TTTCAAAAGGCCGAGTTTCTTTTAGAACATGGTTTTGTAGATCAGATTGTGCCAAGAAAT
                                                                                                    ATCGGTTTTGCTGGCCGCCGTGTAATTGAACAAACGATTCGTCAAGAGTTGCCAGATGAT
                                                                                                                                                                         ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT
                                                                                                                                                                                                            GGTGTTACCGCAAGTTTTGCCGATGGATGGCCGATATTATTTTGGCAGAGCCTCAGAGTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 676 BP; 183 A; 119 C; 190 G; 184 T; 0 other;
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CACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTGGTGAAAAACTGGTGT
                        CATTATCGCAGAGCCAGGGCGATGATAGGCTTTGCGGGGCCTAGGGTGATTAAGCAAAC
                                                 CACTTTTGCGGAACCCGGCGCGCAGATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAAC
                                                                             GCTCTTAAGCGATCCCACTTATGGGGGCGTTAGCGCATCTTTTTGCTTTTTAGGGGATCT
                                                                                             GTATTTGCGCAATCCCACGATGGGTGGGCGCATGGCCTCGTGGGGTTCATCTGGGCATCT
                                                                                                                                 GATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGT
                                                                                                                                                                                   ATTGATTGTTTCAGCGAGTGGGGGGGCTAGGATGCAAGAATCCACTTATTCGCTCATGCA
                                                                                                                                                                                                            GCTGGTCTCCCCTGCTTCCGGTGGTGCGCGCATGCAGGAAGACAATCGAGCTTTTGTCAT
                                                                                                                                                                                                                                         TGTGGAGGGCGAAAAGATCGTAAGAGCAATCAATCGCGCGGTCGCTAAAAGAGAAGCGTT
                                                                                                                                                                                                                                                            GGTCGCGTCGGTGCGCATCATGAAGGCGGATTCACCGCGCCACAGAGCTGAAACTCCCACT
                                                                                                                                                                                                                                                                                            GCGGGCTCGAAGCAAGGCCAAATGCGATGAATCGGTAATTACTGGAGAAGGCACCGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                           AAAATACGAAAAAAGGACTAACCGCCCAAGCTCAGTGATCAGCGGTGAGGCTAAAATCAA
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                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the GC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella GC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC programmes. The antisense nucleic acid sequence is also useful to screen CC programmes. The antisense nucleic acid sequence is also useful to screen CC or homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

CC a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.
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23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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                                                  Sequence
                                                                                                                                    of the printed specification, but was obtained format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; Seq ID No 7288; 511pp; English
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23-MAY-2000;
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                                                                                                                               660 CATTATCGCAGAGCCAGGGGCGATGATAGGCTTTGCGGGGGCCTAGGGTGATTAAGCAAAC 719
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                             12655398
Other_GSSs: AG-ND-133C23.TR
                                                         Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the malaria mosquito Anopheles gambiae mol Genet. Genomics 268 (6), 720-728 (2003)
                                                                                                  Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J., R, C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B., Gardner,M.J. and Collins,F.H.
                                                                                                                                                  Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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CB346970 CAB2SG000
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BZ051213 jnr62h07
BH988285 ocj67b06
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BZ075724 lki53c01
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AQ957569 LERAQ46TF
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Lefebvre

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ACCESSION
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                                                                                             1112113F06.yl C. reir (normalized), Lambda
       BU654446.1
EST.
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Class: BAC ends.
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Tel: 301 838 0208
Fax: 301 838 3543
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partial digest.
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/strain="pEST"
/db xrefe="taxon:7165"
/clone="AG-ND-133C23"
/clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Wector: pECBAC1; Site_1: H: a 86 c 109 g 156 t
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1242 CTCGGCCATCCTTCCGCGACACCAACCACGCGGGAAATCATAGAGCGACAAGGCGT 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                1002 AAACCTGCCGATCGTGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGA 106
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Tel: 919 613 8159
Fax: 919 613 8177
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Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lef
Grossman,A., Chang,C.-W., Silflow,C. and Stern,D.
,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation
Vascular Plants. Project: 1112
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: chauser@duke.edu.
Location/Qualifiers
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                                                                                                                                                                                  GCCCATCATCTCGGTGGTCATTGGCGAGGGCGGCTCGGGCGGCGGCGCTGGCCATTGGCTG 525
                                                                                                                                                                                                                                 GGAGCTGGGCCAGGGCCAGTGCCTGAACCTGCGTGAGATGTTCGGCCTGCGTGT
                                                                             CGCCAACCGCAACCTGATCATGGAGAACGCGGTCTACTACGTGGCCTCGCCCGAGGCCTG 585
                                                                                                                              CGCCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGC 1241
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Strain 21gr cells (CC-1690; mating type plus) and strain 6145c cells (CC-1691; mating type minus) that had been growing on a light-dark cycle (13:11 L/D) in R-medium (Sager and Granick) were separately transfered into nitrogen-free medium at 8 hours into the light period. PolyA mRNA was purified from each sample every 2 hours for the next 18 hours. The mRNA was pooled and used for cDNA synthesis. The cDNA was directionally cloned into lambda Sap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Stratagene) phage. The library was normalized usin method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="C. reinhardtii CC-1690 (mt+), CC-1691 (mt-), Gamete (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2
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/mol_type="mRNA"
/strain="21gr (CC-1690 wild type mt+)
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Pred. No. 2.5e-12;
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Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK 73401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed Eukaryota, mixed EST libraries.

1 (bases 1 to 604)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mjharrison@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2510 Sam Noble Parkway, Ardmore, Tel: 580-223-5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Harrison M.J.
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                                                                                    GTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATTTT
                                                                                                                                                                                                AATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGGCCAAAGGCCAAATGCGATGAATCG
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                                                                                                                                             AATGATGATTATCAAAATCGTCTTGATTCTTATCAAGACAGAACCGGATTACTGGATGCG
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                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                      /Clone lib="WHAM"
/Clone lib="WHAM"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="roots colonized with Glomus versiforme" /dev stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages." /lab host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _Tom_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="MHAM-7I10"
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                                                                                                                                                                                                                                                     Score 84.2; DE Pred. No. 8.3e-0; Mismatches
                                                                                                                                                                                                                                                                               84.2; DB 9;
No. 8.3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grusak, M.A., Samac, D.A., J. and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 713-798-7044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1100 Bates Street,
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                                                                                                                                                                                                                                                                                                                                                           re information is available primer: SKmod (CTA gAA CTA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from developing reproductive tissues of
                                                                                                                                                                                                                                                                                                                                                                                                                 sequence name: MTPAZ34TK information is available
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Immature seeds, collected from pods ranging in a from 11 to 19 days after pollination, were harvested
                                                                                                                 pollination"
                                                                                                                                          /tissue_type="immature seeds"
/dev_stage="Immature seeds, 1
                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="A17"
                                                                                                                                                                                             db_xref="taxon:3880"
clone="pGESD15E20"
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        1 (bases 1 to 1063)
Spencer, D.H., Raymond, C.K., Smith, E.E.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among mu
Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
                                                                                                                                                                                                                                                               pacs1-60 1377.sl pacs1-60 Pseudomonas aeruginosa pacs1-60 1377, genomic survey sequence.
                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                    Pseudomonas aeruginosa
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                                                                                                                                                                                                          Pseudomonas aeruginosa
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  Bacteriol., (
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                                                                                                                                                                                                                                                   GI:27152303
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48.6%;
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Pred. No. 2.5e-11;
0; Mismatches 269;
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                                                            multiple
                                                                                                     Sims, E.E.,
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                                                                                                  Hastings, M.,
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TITLE
JOURNAL
COMMENT
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Best Local Similarity 49.8%;
Matches 206; Conservative
                                                                      AUTHORS
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University of Washington
Box 352145, Seattle, WA 98
Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                  1 (bases 1 to 712)
Grusak, M.A., Samac, D.A.,
,J. and Fraser, C.M.
                                                                                                                      Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                             mRNA sequence.
BI310727
                                                                                                                                                                                                                                                                               EST5312477 GESD Medicago truncatula cDNA clone pGESD8J24 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: craymond@u.washington.edu
                 Unpublished
                                  ESTs from developing reproductive
                                                                                                          Medicago.
                                                                                                                                                                                                                             BI310727.1
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/clone_lib="pacs1-60"
/note="clinical isolate 1-60
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/strain="1-60"
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Pred. No. 6.6e-11;
0; Mismatches 208;
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                                                                    Aken,S.,
                                   of Medicago truncatula
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More information is available at:
Seq primer: Skmod (CTA 9AA CTA gtg
Location/Qualifiers
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Tel: 713-798-7044
Fax: 713-798-7078
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                                                                  TTCCTGGGTCCTCGCGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAG 603
                                                                                                                                                                                                                      ATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGT
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TTTGCAGGTAAAAGAGTAATTGAAGAAACGTTGAAGATCGAAGTGCCCGAAGGTATACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+enriched RNA. The cDNA was directionally ligated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phage using |
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                            241 GATTTTTCCTTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCG 300
                                                                                         181 GAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCC 240
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62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR sequence name: MTPBX17TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA yAAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1100 Bates Street, Houston,
Tel: 713 798 7044
Fax: 713 798 7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Grusak, M.A.
USDA/ARS Children's Nutrition Research
Baylor College of Medicine
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Cheung,F. and Fraser,C.M.
More ESTs from developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mgrusak@bcm.tmc.edu
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Noble EST name: N380393e TIGR sequence name: MTDBW35TK information is available at: http://www.medicago.org
information is available at: http://www.medicago.org
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               /note=TVector: pBluescript SK-; Site_1: EcoRI; S XhOI; cDNA was prepared from polyA+ enriched RNA roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDN directionally ligated into the Unizap XR vector in the CDN directionally ligated into the Unizap XR vector of the control of the Unizap XR vector of 
                                                                                                                                                                                            /tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38"
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                                                                                                                                                                                                                                                                                                                                                                           /mol
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112 c 151 g 265 t
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Pred. No. 1.4e-10;
Mismatches 237;
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1042 bp DNA linear pacs2-164_3167.y3 pacs2-164 Pseudomonas aeruginosa pacs2-164_3167, genomic survey sequence BZ561247 University of Washington Box 352145, Seattle, WA Tel: 2062216954 Whole-Genome-Sequence variation Psedomonas aeruginosa library J. Bacteriol. (2002) In press Spencer,D.H., Raymond,C.K., Smith,E.E., Burns,J.L., Kaul,R. and Olsen,M.V. Fax: 2066857244 Genome Center Contact: Chris K. Raymond Pseudomonadaceae; Pseudomonas. Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonas aeruginosa Pseudomonas aeruginosa BZ561247.1 GI:27180878 Class: shotgun (bases 1 to 1042) craymond@u.washington 1. .1042 Location/Qualifiers /mol_type="genomic organism="Pseudomonas aeruginosa 98105-2145, among multiple isolates USA Sims, E Pseudomonadales; Hastings, M. genomic GSS of. 17-DEC-2002 clone

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RESULT 10
BI725661
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SOURCE
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VERSION
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ORIGIN
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Best Local Sim
Matches 194;
                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                         AUTHORS
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1031080C09.y1 C. reinhardtii
Lambda Zap II Chlamydomonas
                                                                                                                                                                                                                              1 (bases 1 to 539)
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefeby, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                  Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                     DCMB Box 91000
Duke University
                                                                                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
                                                                                                                                                                                       Contact: Charles Hauser
                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                      Vascular Plants. Project: 1031
                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCACCTTGTCCAAGCTTATCGACGCTCCCCTCCCCACCGTTTCGGTCATTATTGGTCAG 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTCCGGCGCGAATTGTCGCAGGCGGCTGAGGAGCTCGGCATCGCAAGCTCGATTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGCGCCGGAAGCCGCCGAGGCCATGGGCATCACCGCCGAGCGCCTGAAAGGCCTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGGTTCCGGCGCGCGCCCATCGGTGTCTGCGACCAGTTGAACATGCTGCAATAC 349
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                                                                                  chauser@duke.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library."
a 320 c
organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164_3167"
/clone=lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic
                                                                  Location/Qualifiers
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reinhardtii CC-1690, Stress II (normalized)
lamvdomonas reinhardtii cDNA, mRNA sequence.
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Pred. No. 2.9e-10;
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REFERENCE
AUTHORS
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KEYWORDS
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ACCESSION
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AG247247
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                                                                                                                     ORGANISM
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Best Local Similarity
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            Lotus japonicus
Lotus japonicus
Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rnsids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                                                                                                                              Lotus japonicus DNA, clone:LjT20k03_not, AG247247
                                                                                                                                                           AG247247.1
GSS.
                                                                                                                                                                                                                                                                                                                                       TCACCTCGGCCGAGCTGGAGGTGAAGTTCGGCGTCATGGACCACATCGTGCCGGA
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Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5') and XhoRI (3')
sites pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

185 c 175 g 84 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:3055"
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Pred. No. 3e-10;
0; Mismatches 2
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REFERENCE

JOURNAL

Sato, S., Nakamura, Y. and Tabata, S. Lotus japonicus TAC End sequences Published Only in Database (2002) 2 (bases 1 to 652)

TITLE

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RESULT 12
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Matches 222;
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                                      AUTHORS
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Direct Submission
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:ssatc@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
                                                                                                                                                                                        CB977199 617 bp mRNA linear CAB40003 IVa Ra D11 Cabernet Sauvignon Berry - CF CDNA clone CĀB40003_IVa_Ra_D11 3', mRNA sequence. CB977199 CB977199.1 GI:30300405
                                                                          Spermatophyta; Magnoliophyta; vitaceae; Vitis.
                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
                                                                                                                                  Vitis vinifera
Vitis vinifera
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Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGTATTCCTGTAGCAATTGGGATTATGGATTTTGAGTTTATGGGAGGTAGTATGGGAT 131
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                                      da Silva, F., Iandolino, A., Lim, H.,
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/clone_lib="genomic TAC library"
/note="VECTOR:pYLTAC7"
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/strain="Miyakojima MG-20"
/db_xref="taxon:34305"
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/mol_type="genomic DNA"
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Pred. No. 5.2e-10;
0; Mismatches 219;
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Research; 2-6-7
                                      Baek, J., Jones, K.
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One Shields Ave, Davis, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
Contact: Douglas Cook,
CAES Genome Facility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 530 754 6617
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                                                                                                                                                                                              GCGCATTTGCCGTTCCTGGTGTATTTGCGCA---ATCCCACGATGGGTGGCGCCATGGCC 489
                                                                                                                                                                                                                                      ACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCGCGCATGCAGGAA 372
                                                                                AGTTTTGGTATGTTGGGAGATATCATTATTGCCGAACCCAATTCCTACATTGCATTTGCG
                                                                                                                      TCGTGGGGTTCATCTGGGGATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGTTTCCTG
                                                                                                                                                            AATAAAAAGTTATTTTATGTATCAATCCTTACATCTCCTACTACTACTGGTGGGGTGACAGCA
                                                                                                                                                                                                                                                                          GACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAG 432
                                                                                                                                                                                                                                                                                                                    ACCAATGAATTTCTACCTCTTATTTTAGTGTGTTCTTCCGGAGGAGCACGTATGCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAGGCACAGGTCAACTAAACGGTATTCCCGTAGCAATTGGGGTTATGGATTTTCAGTTT
        GGTAAAAGGGTAATTGAACAAACATTGAAAAAGACAGTACCTGAAGGTTCACAAGCGGCT
                                          GGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCG 609
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primer: GCCAAACGAATGGTCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / clone lib="Cabernet Sauvignon Berry - CAB4"
//clone lib="Cabernet Sauvignon Berry - CAB4"
//clone lib="Capernet Sauvignon Companies of Vitis Vinifera cv.
Sfil; CAB4 is a cDNA library of Vitis Vinifera cv.
(Cabernet Sauvignon' Clone 8 berries. Sampled berries were collected from field-grown vines during stage II of berry growth (berries were green and hard) at approximately 60 days after full bloom. The average berry size was 9 milimeters. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5'and 3' adaptors were used in cloning as follows:
5'-ANGCAGTGGTATCAACGCAGAGTGGCCATTACGGGG-3' and 5'-ARGCAGTGGAGCCGAGAGTGGCCAATTACGGCCGG-3' and 5'-ARTCTAGAGCCGAGGCGGAGCAGG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Hermaphrodite"
/dev stage="Berry on stage II,
/lab_host="DH5alpha"
clone lib="^~~
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/cultivar="Cabernet Sauvignon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db xref="taxon:29760"
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47.8%;
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Pred. No. 2.6e-09;
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   BZ035752
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Genome Project: Generation of a Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee,N.H., Glodek,A., Chandra,I., Mason,T.M.,
Kerlavage,A.R. and Adams,M.D.
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                                                                                                                        TGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCG 481
                                                                                                                                                       TGTCGCTGATGCAGATGGCGAAAACCTCTGCGGCACTGGCAAAAATGCAGGAGCGCGGCT
                                                                                                                                                                                         GAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAGGCGCATT
                                                                                                                                                                                                                           ATAACTGCCCGCTGATCTGCTTCTCCGCCTCTGGTGGCGCACGTATGCAGGAAGCACTGA 308
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                                                                                                                                                                                                                                                                                                                                                                  AAGGCACTCTGTATGGAATGCCGGTTGTCGCCTGCGGCATTCGAGTTCGCCTTTATGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                   GAATATTTATTCCATAAGGGCTTATTCGATTTAATCGTACCAC 94
                                                                                      TGCCGTACATCTCCGTGCTGACCGACCGACGATGGGCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medical Center Drive,
(301)-838-3529
(301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="ATCC (inhost);2036524"
/db_xref="taxon;10118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Rattus sp."
/mol_type="mRNA"
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Pred. No.
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Bento Soares Rattus
   DNA
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Class: shotgun
High quality sequence start: 8
High quality sequence stop: 551.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine Email: submissions@watson.wustl.edu Plate: oeh49 row: c column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., ,W., Rabinowicz,P.D. and Wilson,R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whole genome shotgun reads from Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica oleracea
TGGGTCCTCGCGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                 TTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATTTTTCCT
                                                                                                    CAAGTAAAAAGGTATTCTATATCAATTCTTACATCTCCTACTACCGGTGGGGTGACAG
                                                                                                                                                                                                       AAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCG
                                                                                                                                                                                                                                                                            CCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCGCGCATGCAGG
                                                                                                                                                                                                                                                                                                                                               TCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTCACCGCG
                                                                                                                                                                                                                                                                                                                                                                                 AAACAGGTACAGGTCAATTAAACGGTATTCCGGTAGCTCTTGGGGGTTATGGATTTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGCAAAGGCCAAATGCGATGAATCGGTAA 190
                                  CAAGTTTTGGTATGTTGGGGGATATCATTATTGCCGAACCCTATGCCTACATTGCATTTG
                                                                  ccrcereeegrrcarcreeecarcreacrrreeegaaccceecececaaraeerrrec
                                                                                                                                     AGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAA---TCCCACGATGGGTGGCGCCATGG
                                                                                                                                                                     AAGGAÄGTTTAAGTTTGATGCAAÄTGGCTAAAATTTCTTCGGTTTTATGTGATTATCAAT
                                                                                                                                                                                                                                        CTACCAATCAATATTTACCTCTTATTTTAGTGTGTTCTTCCGGAGGAGCACGAATGCAAG
                                                                                                                                                                                                                                                                                                              TTATGGGGGGTAGTATGGGATCCGTAGTAGGCGAAAAAATAACTCGTTTGATCGAGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Brassica oleracea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73.8; DB 28;
Pred. No. 5.7e-09;
D; Mismatches 283;
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Gaps

483

250 423

243 430

303 370 363 310

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RESULT 15
CB346970
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                                                                                                                                                                       BASE COUNT
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136 TATGCAGAGACCTTGGAGCGGGCTCGAAGCCAAGGCCAAATGCGATGAATCGGTAATTACT 195
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                                                                             248;
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CB346970
CB325G0002 IVaF CO2 Cabernet Sauvignon Berry - CAB2SG Vitis
Vinifera cDNA clone CAB2SG0002 IVaF CO2 5', mRNA sequence.
CB346970
CB346970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
On Mar 14, 2003 this sequence version replaced gi:28967937
Contact: Douglas Cook, PhD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; Vitaceae; Vitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: ACGGTACCGGACATATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAES Genome Facility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tags from cabernet sauvignon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: drcook@ucdavis.edu
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                                                                                                   Similarity
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530 754 6617
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                                                                             Conservative
                                                                                                                                                                                      /lab host="DH5alpha"
//clone lib="Cabernet Sauvignon Berry - CAB2SG"
//clone lib="Cabernet Sauvignon Berry - CAB2SG"
//note="Organ: Berry; Vector: pDNR; Site_1: SfiI; Site_2:
/note="Organ: Berry; Vector: pDNR; Site_1: SfiI; Site_2:
/note="Organ: Berry; Vector: pDNR; Site_1: SfiI; Site_2:
/note="Organ: Berry; Vector: pDNR; Site_1: Sauvignon Clone
8 berries were collected at veraison (transition between stage II and stage III of berry growth) from field-grown vines 60 days after full bloom. Berries were still green but soft. Sampled vines were located at the University of California, Davis, experimental vineyard. CDNAs were made by oligo-dT priming and directionally cloned. 5'and 3' adaptors were used in cloning as follows: 5'-ANGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and 5'-ATTCTAGAGCCCGAGCGGCGACATG-GT (30) NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

85 a 102 c 130 g .188 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CAB2SG0002 IVaF_C02"
/sex="Hermaphrodite"
/dev_stage="Veraison"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:29760"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cultivar="Cabernet Sauvignon"
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O
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                                                                                                 5.0%;
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                                                                           0;
                                                                                                   Score 73.6; DB 14;
Pred. No. 6.2e-09;
                                                                             Mismatches
                                                                                269;
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Search completed: November 13, 2003, 02:26:32 Job time: 3245.57 secs

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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

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EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1999-05 NUMBER OF SEQ ID NOS: 3 SOPTWARE: PatentIn Ver. 2.1 SEQ ID NO 2 LENGTH: 1473 TYPE: DNA ORGANISM: COTYNEBACTERIUM 9 FEATURE: LOCATION: (1)(1473) OTHER INFORMATION: accDA -09-362-899-2 Query Match Best Local Similarity 100.0 Matches 1473; Conservative 1 GTGGAGAAGCGTTTTCC	28 54.6 3.7 3183 1 US-08-849-212-3 29 51 3.5 2894 1 US-08-278-091-1 31 51 3.5 2894 1 US-08-472-173-1 31 51 3.5 2894 1 US-08-472-173-1 32 51 3.5 2894 2 US-08-472-173-1 33 51 3.5 2894 2 US-08-487-167-1 34 51 3.5 2894 2 US-08-26-149-1 35 51 3.5 2894 2 US-08-26-149-1 36 51 3.5 2894 2 US-08-26-149-1 37 51 3.5 2894 2 US-08-801-499-1 38 51 3.5 2894 3 US-09-074-660-1 39 51 3.5 2894 3 US-09-074-660-1 39 51 3.5 2894 3 US-09-074-660-1 40 51 3.5 2894 3 US-09-106-468-1 41 51 3.5 2894 3 US-09-106-468-1 42 49.8 3.4 789 4 US-09-106-468-1 43 48.2 3.3 984 1 US-09-106-468-1 44 48.2 3.3 984 2 US-08-611-107-11 45 48.2 3.3 984 2 US-08-611-107-11 46 48.2 3.3 984 2 US-08-611-107-11 47 48.2 3.3 984 2 US-08-611-107-11 48 48.2 3.3 984 2 US-08-611-107-11 49 48.2 3.3 984 2 US-08-611-107-11 40 51 3.5 2894 3 US-09-106-468-1 41 48.2 3.3 984 1 US-08-611-107-11 42 49.8 3.4 789 4 US-09-106-468-1 43 48.2 3.3 984 2 US-08-611-107-11 44 48.2 3.3 984 1 US-08-611-107-11 45 48.2 3.3 984 2 US-08-611-107-11 46 48.2 3.3 984 3 US-09-106-468-1 47 48.2 3.3 984 3 US-09-106-468-1 48 48.2 3.3 984 1 US-08-611-107-11 49 48.2 3.3 984 2 US-08-611-107-11 40 51 3.5 Sequence 1 41 48.2 3.3 984 2 US-08-611-107-11 42 49.8 3.4 789 4 US-09-106-468-1 43 48.2 3.3 984 1 US-08-611-107-11 44 48.2 3.3 984 1 US-08-611-107-11 45 48.2 3.3 984 2 US-08-468-793-11 46 48.2 3.3 984 2 US-08-468-793-11 47 49.8 3.4 789 4 US-09-106-468-1 48 51 3.5 Sequence 11 49 49.8 3.4 789 4 US-09-106-468-1 40 51 3.5 Sequence 11 41 49.8 3.4 789 4 US-09-106-468-1 42 49.8 3.3 984 2 US-08-611-107-11 43 48.2 3.3 984 1 US-08-611-107-11 44 48.2 3.3 984 1 US-08-611-107-11 5 Sequence 11 45 49.8 3.4 789 4 US-09-106-468-1 48 52 3.3 984 1 US-08-611-107-11 5 Sequence 11 49 49.8 3.4 789 4 US-09-106-468-1 5 Sequence 11 40 51 3.5 Sequence 11 41 51 3.5 Sequence 11 42 49.8 3.4 789 4 US-09-106-468-1 43 48.2 3.3 984 2 US-09-106-468-1 44 48.2 3.3 984 1 US-09-106-468-1 5 Sequence 11 5 Seq
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APPLICANT: Degussa-H1s AG
APPLICANT: Degussa-H1s AG
APPLICANT: Forschungszentrum-Jlich GmbH
APPLICANT: FORSChungszentrum-Jlich GmbH
ITILS OF INVENTION: PROCESS FOR THE PREPARATION OF
CURRENT APPLICATION NUMBER: US/09/362,899
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: DE 19924365.4
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2123
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US-09-362-899-1
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LOCATION: (508)..(1980)
OTHER INFORMATION: accDA
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ORGANISM: Corynebacterium
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; Sequence 2, Application US/09103840A
Patent No. 6294328
; GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WRASER, Claire M.
APPLICANT: WRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FO
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CURRENT APPLICATION NUMBER: US/09/103,
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver: 2:1
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APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
S-09-103-840A-1
                                                                                                                                            Query Match 21.2%;
Best Local Similarity 54.0%;
Matches 717; Conservative
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                  ACCGGGTGCTGGCCGCACTCCACGGCTGGCTGGCGCCCTTGCCCCGAAGGAGCCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                              GGGGCCGGCCCGTGGTGCTGATTGGGCAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACCGATGCTGGATCGTGCGTTGACGGTGCTCATCGACGCTCCCGAACCGCTTCCCGGCAC 1007488
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                                                      ATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCTCGG
                                                                                                                              CCGTTTCGGTCATTATTGGTCAGGGCGTTGGCGGTGGCGCTGGCCATGCTGCCCGCCG
                                                                                                                                                                 GCGGGCTGGCCGGATCGCGCATTGCCTGGCCGAGCTCGTCACGCTGGATACCCCGA
                                                                                                                                                                                                                                                            TGCCGATCGTGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCAACAACTCCTGGCGTGGCA---CTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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GENERAL INFORMATION:
                                                                                                                                                       Matches
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/720-2441 INFORMATION FOR SEQ ID NO: 140:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS TITLE OF INVENTION: DIAGNOSTICS AND THERAPPUTICS NUMBER OF SEQUENCES: 411

CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: CO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SMITH, DOU
APPLICANT: MAO, JEN-I
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                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: BOSTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                      Local
                                                                                                               178 GATGAATCGGTAATTACTGGAGAGGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTG
                                                                                                                                                       296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02210
                                                                                                                                                                   Similarity
GCGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGT 357
                                                          GACGAATCGGTGCTGACCAGCCAGGGGTGCGTATTCGGGCGACGGGTAGCGATAATTGTC
                              TGCAAATTCAGCTTCCTCGGTGGCCGTATCGGGGTGGCAGCCGCGGAGCGAATCACCGCC
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                                                                                                                                                                Score 142; DB 4; Length 36063; Pred. No. 1.3e-29;
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AGCGTCACCGCGAGGCGCATTTGCCGTTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG 478
                                                                                       CGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGC 418
                                                                                                                                                  CGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCCTGCTTCCGGTGGTG 358
                                                          CGCGCATGCAGGAAGCGCTGATCTCGCTGATGCAGATGGCCAAGACCTCGGCGGTCCTGG 712
                                                                                                                    CAGCCAACGTCGCCCTGGAGAAGCGCTGCCCGCTGATCTGCTTCTCCGCCTCCGGCGCGCG 652
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; TYPE: DNA ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-12180
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US-09-252-991A-12180
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PRIOR FILING DATE: 1998-07-27
RUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12180
                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINI
TITLE OF INVENTION: AERUGINOSA FOR DIAGNO:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
239 CCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGG 298
                                                        AGGACGCGCTGATCGCCATGAGCGGCAAGCTGCAGGGTATGCCGGTGGTCGCCTGCGCCT 532
                                                                                               ATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGT
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    J. Rubenfield et al.
    ON: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS 107196.136

                                                                                                                                                                                                    7.9%;
52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 60/094,190
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                                                                                                                                                                   Score 116.4; DB 4;
Pred. No. 4.2e-23;
0; Mismatches 241;
                                                                                                                                                                      Indels
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RESULT 7
US-09-252-991A-12415/c
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-19
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SEQ ID NO 12415
LENGTH: 1338
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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TAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTG
                                                                                                                        GCGTTTCCGCCAGCCTGGCGATGCTCGGCGACGTGATCGTCGGCGAACCCCAAGGCGCTGA
                                                                                                                                                               GCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGA
                                                                                                                                                                                                          AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG
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                                        TCGGCTTCGCCGGTCCCCGCGTGATCGAGCAGACCGTCCGCGAGAAGCTGCCGGAAGGCT
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CURRENT APPLICATION NUMBER: US/09/773,816
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 60/179,305
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 611;
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TITLE OF INVENTION: NON-STEROIDAL
TITLE OF INVENTION: ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(23623)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Human
FEATURE:
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  CCAATTGCGTGCAGCGGTGG--
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                                                                                                                                                                                                                                                                                           CGGGCAACTGGACGAGGCCGGCGTGTTGACCATCTCGCTGGTCACCGACCCCACCTACGG
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                                      GTTCCAGACCGCCGAATACCTCCTCGAACACGGCCTGATCGACCTGATCGTGCCGCGCCC
                                                                             TCTCGGCTTCGCCGGCCGGCGGGTCATCGCGCAGACCATCCGCGAGGAACTGCCGCCGGA
                                                                                                                                                               GATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGG 596
                                                                                                                                                                                                          CGGCGTCGCGGCGTCCTTCGCGACCCTGTGCGACGTCATCGTCGCCGAACCCGGCGCGCG
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                                                                                                                                                                                                                                                                                                                                GCAGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGG
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46.68;
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Pred. No. 2.7e-20;
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    -CAAAAACCC 685
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RESULT 9
US-09-107-532A-170
US-09-107-532A-170
; Sequence 170, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: OF INVENTION: NUCLEIC ACID
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7477
                                                                                                                                                                  NUMBER OF SEQUENCES: 7310
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    COMPUTER READABLE FORM:
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                                                              STATE: Massachusetts
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                         COUNTRY: USA
ZIP: 02354
                                                                                      CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAGCTAAACCTGCCGATCGTGTCCATCGACACCTCCGGCGCCGAATTGTCGCAGGC 1055
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                                                                                                                                                                                       ENTEROCOCCUS
                                                                                                                                                                                   and David Bush
AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 170:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/107,53
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...870
SEQUENCE DESCRIPTION: SEQ ID NO: 170:
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ORGANISM: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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AATTG 663
                                                                                                                                                         TAGGITTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTG
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                                      TCCAAAAGGCTGAATTCTTATTATCTCATGGTTTTGTCGATCAGATTGTTCCCCGCATGG
                                                                             TCGGTTTTGCTGGAAGACGCGTCATCGAACAGACGATCAAGCAGGAACTTCCAGAAGATT
                                                                                                                                                                                                         GAGTAACTGCCAGTTTTGCAATGGAAGGCGATATTATTCTAGCAGAACCCCAAAGCTTGA
                                                                                                                                                                                                                                               GCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGA
                                                                                                                                                                                                                                                                                      AACGGCATAGCAATGAAGGTCTTTTTTATCTAACTGTTTTAACGGACCCGACGACCGAG
                                                                                                                                                                                                                                                                                                                             AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: <Unknown>
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50.9%;
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Pred. No. 1.1e-19;
0; Mismatches 238;
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RESULT 11
US-08-961-527-7/c
US-08-961-527-7/c
; Sequence 7, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12365
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LENGTH: 444
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Best Local Similarity
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APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER: OF SEQ. ID NOS: 33142
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                              APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep
NUMBER OF SEQUENCES: 391
                CORRESPONDENCE
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Human Genome Sciences,
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Pred. No. 7.3e-18;
0; Mismatches 208; Indels
                                                pneumoniae Polynucleotides
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                                                  Sequences
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Best Local Similarity
Matches 248; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER
FILTER
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LENGTH: 19702 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. Ar REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGATTCTAACTTTATCATGGCTTCTATGGGTACGGTTGTAGGTGAAAAATCACTCGTT 11434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGG 298
                                                                                                                                                                          TAGGTTTTCCTGGGTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTG 598
                                                                                                                                                                                                                                                                                      AACGCCATTCAAATGCTGGTCTCTTTACCTGACCATTTTGACAGATCCAACGACTGGTG 1125
                                                                                                                                                                                                                                                                                                                                                                                         CGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTG 358
                                                                                                                                                                                                                 GTGTGACAGCTTCTTTCGCTATGGAAGGCGATATCATTCTGGCTGAACCACAGAGCTTGG 11194
                                                                                                                                                                                                                                                                                                                                                         CCCGTATGCAGGAAGGAATCATGAGTCTCATGCAGATGGCTAAGATCTCTGCGGCGGTTA 11314
                                                                                                                                                                                                                                                                                                                                                                                                                                TGTTTGAGTATGCGACTGTCGAAAAATTGCCAGTTGTCCTATTCACAGCCTCTGGTGGAG 11374
ACTTACCAGATACGATTGCTA 11053
                                 AATTGCGTGCAGCGGTGGCAA 679
                                                                   TCCAAAAGGCAGAATTCCTATTAGAACATGGCTTTGTGGATGCTATTGTCAAAAGAAGAG 11074
                                                                                                      TTGGTTTTGCTGGGCGTCGTGTGATTGAAAATACGGTTCGTGAAAGCTTGCCTGAGGATT
                                                                                                                                                                                                                                                 GCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAAACCCGGCGCGCAGA 538
                                                                                                                                                                                                                                                                                                                    AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG 478
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49.5%;
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Best Local Similarity
Matches 248; Conserv
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Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
      1337280
                                                                                1337220
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                                                                                                                                                                                                                                                                                                              1337040
                                                                                                                                                                                                                                                                                                                                                                                       1336980 AAGATGCGCTAATTACTATGACAGGTACACTTTATAATATGCCAATCGTTGTGGCTGCAT 1337039
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FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
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ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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GCGTATCAGCCAGTTTTGCGATGTTAGGGGATTTTAAATATTGCCCGAGCCAAAAAGCCTTAA, 1337339
                                      GCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGA, 538
                                                                                                                 AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG
                                                                                                                                                       CTCGTATGCAGGAAGCATTATTCTCTTTAATGCAAATGGCAAAAACTAGTGCCGTACTTG 1337219
                                                                                                                                                                                           CGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGC
                                                                                                                                                                                                                                  CGGCTGAAAAAGCGATGGAAATGAATTGTCCATTTGTGTGTTTCTCTGCGAGTGGTGGTG
                                                                                                                                                                                                                                                                      CGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTG
                                                                                                                                                                                                                                                                                                            CGAACTTTGCTTTTATGGGCGGTTCAATGGGTTCTGTAGTTGGTGCAAAATTTGTTAAAC 1337099
                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGT
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OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
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ilarity 49.5%;
Conservative
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Pred. No. 5.7e-16;
0; Mismatches 253;
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US-09-643-990A-1
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                                                                       Query Match
Best Local Similarity
Matches 248; Conserv
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GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
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                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
1336980 AAGATGCGCTAATTACTATGACAGGTACACTTTATAATATGCCAATCGTTGTGGCTGCAT 1337039
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186F10
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TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
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J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome,
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                 LENGTH: 1830121 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                ATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCCGGTAGCCCGTTATTTTGT 238
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STREET: 9410 Key West Avenue
                                                                         Conservative
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                                                                     Score 96.2; DB 4;
Pred. No. 5.7e-16;
0; Mismatches 253;
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                                                                                                      Length 1830121;
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239 CCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGG 298

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US-09-347-878-25
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TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Applicate Patent No. 6376210
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (1131)..(2399)
OTHER INFORMATION: Escherichia coli nucleic acid encoding
OTHER INFORMATION: folypolyglutamate synthetase-dihydrofolate
OTHER INFORMATION: synthetase
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: M32445/GenBank
-09-347-878-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Escherichia coli
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                                        TGAAACTCCCACTGCTCCCCCTCCTTCCCGTGGTGCGCGCATGCAGGAAGACAATC
                                                                                 GTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTCACCGCGCCACAGAGC
                                                                                                                                                                   AAGGCACTCTGTATGGAATGCCGGTTGTCGCTGCGGCATTCGAGTTCGCCTTTATGGGCG
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OTHER INFORMATION: Predicted region encoding membrane bound portion
OTHER INFORMATION: of the mps gene product. "n" is any of a, t, c of the manual of the mps gene product. "n" is any of a, t, c of the mps gene product.
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EARLIER APPLICATION NUMBER: POT/JP97/01043
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1997-03-27
EARLIER FILING DATE: 1997-03-27
EARLIER FILING DATE: 1996-03-28
EARLIER APPLICATION NUMBER: JP 8-146833
EARLIER FILING DATE: 1996-05-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 2
rength: 954
                                                                                                                            Matches
                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: FINE MAGNETIC PARTICLES CONTAINING USEFUL PROTEINS TITLE OF INVENTION: BOUND THERETO, PROCESS FOR PRODUCING THE SAME, AND TITLE OF INVENTION: THEREOF PILE REFERENCE: MATSUNAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KAMIYA, Shinji APPLICANT: NAMBA, Kenryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MATSUNAGA, Tadashi
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 95
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  1011 GATCGTGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGCTCGG 1070
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                                                             813 YMGNAAYCCNGAYYTNATGATGCARACNYTNWS 845
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                                                                                                                                                                                                                                                                633 NGTNYTNATGYTNGARCAYGCNATHTAYWSNGTNATHWSNCCNGARGGNTGYGCNWSNAT 692
                                                                                                                                                                                                                                                                                                                                                                                               513 NCARGCNGARGCNATHGCNMGNWSNATHGARACNTGYYTNAAYGTNMGNGTNCCNYTNGT 572
                                                                                                                             753 RGAYYTNCAYAARYTNWSNATHATHGAYWSNGTNGTNCCNGARCCNATGGGNGGNGCNCA 812
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1473
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L: /cgn2_6/ptodata/2/pubpna/US07_
2: /cgn2_6/ptodata/2/pubpna/PCT_b
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/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1 14		100.0	1473	10 1	US-09-738-626-929
	2 1473		100.0	1473	13	US-10-024-370-2
	3 14		100.0	2123	13	US-10-024-370-1
ი	4 14		100.0	3309400	10	US-09-738-626-1
	5 312		21.2	1488	10 1	US-09-712-363-35
	6 122	80	8.3	873	9	'S-09-815-242-7
	7 1	21	8.2	867	9	US-09-815-242-6828
	8	21	8.2	6021	10	US-09-070-927A-
	9 119	'n	8.1	870	9 U	US-09-815-242-7288
_	10 119.2	N	8.1	1053	10	US-09-895-913A-97
_	11 108	80	7.3	993	9 U	IS-09-815-242-9
_	12 102	89	7.0	915	9	US-09-815-242-6133
_	13 97	80	6.6	867	9	US-09-815-242-9520
_	14 96.8	80	6.6	654	10 1	US-09-974-300-5531
_	15 96	'n	6.5	891	9	US-09-815-242-7115
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US-10-289-757-44	US-10-162-497-7	US-10-156-761-7101	US-10-156-761-2173	US-09-815-242-4026 .	US-09-841-132-461	US-10-003-446-14	US-09-767-479-11	US-10-156-761-3330	US-09-815-242-2856	US-10-156-761-3349	US-09-815-242-9521	US-09-815-242-9268	US-09-815-242-9799	US-09-815-242-5951	US-09-070-927A-269	US-09-974-300-1085	US-09-815-242-3909	US-09-815-242-6829			4 US-10-156-761-1		US-09-815-242-7836	US-08-781-986A-312	US-09-815-242-4369	US-09-815-242-8520	US-09-815-242-9267
Sequence 44, Appl	Sequence 7, Appli	Sequence 7101, Ap	Sequence 2173, Ap	Ξ.	Sequence 461, App	Sequence 14, Appl	Sequence 11, Appl	•	Sequence 2856, Ap	3349,	Sequence 9521, Ap	Sequence 9268, Ap		•	Sequence 269, App	Sequence 1085, Ap		Sequence 6829, Ap	Sequence 1, Appli	Sequence 3318, Ap	Sequence 1, Appli	Sequence 5702, Ap		Sequence 312, App	4369	Sequence 8520, Ap	Sequence 9267, Ap

ALIGNMENTS

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; LENGTH: 1473 ·
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-929
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US-09-738-626-929
; Sequence 929, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
                                                                                                                                        FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
                                                                 SOFTWARE: PatentIn ver.
SEQ ID NO 929
LENGTH: 1473
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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Query Match Best Local Similarity Matches 1473; 100.0%; Score 1473; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches DB 10; <u>,,</u> Indels Length 1473; ,. Gaps

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                                                                     ATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGCTCGGCATCGCAAGC
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APPLICANT: SAHM, HERMANN
APPLICANT: SAHM, HERMANN
APPLICANT: MOCKEL, BETTINA
ITILE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY
ITILE OF INVENTION: FERMENTATION AND NUCLEOTIDE SEQUENCES CODING FOR
ITILE OF INVENTION: accDA GENE
FILE REFERENCE: 21133-284139-MAS
CURRENT APPLICATION NUMBER: US/10/024,370
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/362,899
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
INUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 1473
TYPE: DNA
COTYNIEM: COTYNEBACTERIUM Glutamicum
                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1473)
OTHER INFORMATION: accDA
US-10-024-370-2
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US-10-024-370-2
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Best Local S
Matches 1473
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APPLICANT: ELKMANNS, BERND
APPLICANT: EGGELING, LOTHAR
APPLICANT: SAHM, HERMANN
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Sequence 1, Application US/10024370

Publication No. US20020142405A1

GENERAL INFORMATION:

APPLICANT: TILG, YVONNE

APPLICANT: ELKMANNS, BERND

APPLICANT: EGGELING, LOTHAR

APPLICANT: EGGELING, LOTHAR

APPLICANT: MOCKEL, BETTINA

TITLE OF INVENTION: PERCESS FOR THE PREPARATION OF L-AMINO ACIDS BY

TITLE OF INVENTION: FERNENTATION AND NUCLEOTIDE SEQUENCES CODING FOR

TITLE OF INVENTION: accDA GENE

TITLE OF INVENTION: accDA GENE

TITLE OF INVENTION: accDA GENE

TITLE OF INVENTION NUMBER: US/10/024,370

CURRENT APPLICATION NUMBER: US/10/024,370

CURRENT APPLICATION NUMBER: 09/362,899

PRIOR APPLICATION NUMBER: 09/362,899

PRIOR APPLICATION NUMBER: DE 199 24 365.4

PRIOR APPLICATION NUMBER: DE 199 24 365.4

PRIOR APPLICATION NUMBER: DE 199 27-29

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
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; FEATURE:
; NAME/KEY: gene
; LOCATION: (508)...(1980)
; OTHER INFORMATION: accDA
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APPLICANT: ANALY, SCANO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TAYEISHI, NACKO
APPLICANT: TAYEISHI, NACKO
APPLICANT: TAYEISHI, NACKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: J99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATCHIN DATE: 3.0
SEQ ID NO 1
TENCTURE 3000.00
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
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US-09-738-626-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1473; Best Local Similarity 100.0%; Pred. No. 0; Matches 1473; Conservative 0; Mismatches
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
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ANDO, SEIKO
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; ORGANISM: Mycobacterium
US-09-712-363-35
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Patent NO. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio
APPLICANT: Marcotte, Edward
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US-09-712-363-35
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PRIOR PILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR PILING DATE: 1999-02-01
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR PILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR APPLICATION NUMBER: 60/165,066
PRIOR PILING DATE: 1999-11-12
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Best Local Similarity
Matches 717; Conserv
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CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
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APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
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                                                              ACAACCAGGCGCCTGCCCTACCTGGTCTATTTGCGCCATCCGACCACGGGTGGAGTTT
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                                                                                     Sequence 7800, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
   APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith WAPPLICANT: Wall, Daniel APPLICANT: Trawick, John D.
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Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION UMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-12-22
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Best Local S
Matches 265
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 7800
LENGTH: 873
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Local Similarity 52.8%;
les 265; Conservative
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Pred. No. 1e-27;
0; Mismatches 237;
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RESULT 7 US-09-815-242-6828

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; TYPE: DNA; CORGANISM: Enterococcus f; FEATURE; ; NAMEKEY: CDS; LOCATION: (1)...(867) US-09-815-242-6828
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 6828
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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FILING DATE: 2000-05-26
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ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT 597
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                                 GGTGTTACCGCAAGTTTTGCGATGGATGGCGATATTATTTTGGCAGAGCCTCAGAGTTTA
                                                                   CAACGGCATAACAAAGCAGGCTTGCTGTATCTTACGGTATTGACTGATCCAACGACTGGC
                                                                                                                                    CAGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGT
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carr, Grant J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 3.7e-27;
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RESULT 8
US-09-070-927A-458
(Sequence 458, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID US-09-070-927A-458
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                                                                                                                                                  Best Local Similarity Matches 259; Conserv
                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
5381 ATGGACGCTAATTTTATCATGGGCAGTATGGGGAACGATTGTTGGTGAAAAAATCACACGC 5440
                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 6021 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kenley K. Hoover REGISTRATION NUMBER: 40,3
REFERENCE/DOCKET NUMBER: 3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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Patrick J. Dillon
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                   238 TCCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCGCATCATGAAG 297
                                                                                                          178 GATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTG 237
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                                                                         GATGAAGCTGTCTTAACGGGAGAAGCAACAATTGAAGGACAAGCTGTTGCAATTGGAATC
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OPERATING SYSTEM: MSDOS ve
SOFTWARE: ASCII Text
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ilarity 53.0%;
Conservative
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                                                                                                                                                                    Score 121; DB 10;
Pred. No. 7.9e-27;
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                                                                                                                                                  230;
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                                                                                                                                                                    SEQ ID NO 7288
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR PRIOR DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu. H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 60/242,578
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                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-02-16
                                                                                                          TYPE: DNA
ORGANISM: Helicobacter
                                                         NAME/KEY: CDS
LOCATION: (1)
                                                                                          FEATURE:
                                                                                                                                             ENGTH: 870
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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Zyskind, Judith W.
                                                    ... (870)
                                                                                                            pylori
   8.1%;
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     Score 119.2;
     DВ
     9;
   Length 870;
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; NAME/KEY: CDS
; LOCATION: (110)...(976)
US-09-895-913A-97
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Matches 283; Conserv
                                                                              SEQ ID NO 97
LENGTH: 105
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                   Sequence 97, Application US/09895913A Patent No. US20020160456A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                          PILE REFERENCE: 06.12/043002
CURRENT APPLICATION NUMBER: US/09/895,913A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
                                                                                                                                                                                                                                      APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kleanthous, Harold
                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                 ORGANISM: Helicobacter
                                                FEATURE
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Miller, Charles
Tomb, Jean Francois
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RESULT 11
US-09-815-242-9854
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               PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                      Sequence 9854, Application US/09815242 Patent No. US20020061569A1
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Best Local
                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                   TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                              APPLICANT: Haselbeck,
APPLICANT: Ohlsen, K
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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                                                                                                                                                                                                              Xu, H. Howard
                                                                                                                                                                                                                          Yamamoto, Robert T.
     DATE:
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Pred. No. 1.4e-26;
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
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US-09-815-242-6133
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                                                                                                                         Sequence 6133, Application US/09815242 Patent No. US20020061569A1
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Carr, Grant J. Yamamoto, Robert Xu, H. Howard

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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 9854
LENGTH: 993
TYPE: DNA
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Best Local Similarity 49.6%;
Matches 276; Conservative
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NAME/KEY: CDS
LOCATION: (1).
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                               CGGTGGCAAAAACCCT
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Pred. No. 4.5e-23;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR PELIOR DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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Best Local S
Matches 275
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NAME/KEY: CDS
LOCATION: (1).
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SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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TYPE: DNA
ORGANISM: Escherichia
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                                                                       GCGTGGCACTTCCGGTGATGGA 761
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TAGTGGTÁCCCCCGGTACCGGA 896
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Pred. No. 1.8e-21;
0; Mismatches 287;
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US-09-815-242-9520
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CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR FILLING DATE: 2000-05-27
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
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Patent No. US2002
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Best Local Similarity
Matches 249; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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LOCATION: (1)
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                                                                                                                                                                                                                                                                                                              TGGATTCTAACTTTATCATGGCTTCTATGGGTACGGTTGTAGGTGAAAAATCACTCGTT
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                                           GCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGA 538
                                                                                                                                                                                                                                 CGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGC
                                                                                                                                                                                                                                                                                 TGTTTGAGTATGCGACTGTCGAAAAATTGCCAGTTGTCCTATTCACAGCCTCTGGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAGCCGTTGTGACAGGAACTGCTCTTATTAAAGGTCAGACTGTGGCTCTTGGGATTA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGT
                                                                                                                                     <u>AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG</u>
                                                                                                                                                                                   CCCGTATGCAGGAAGGAATCATGAGTCTCATGCAGATGGCTAAGATCTCTGCGGCGGTTA
GTGTGACAGCTTCTTTCGCTATGGAAGGCGATATCATTCTGGCTGAACCACAGAGCTTGG
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Trawick, John D.
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0020061569A1
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Pred. No. 6.6e-20;
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631

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LENGTH: 654

TYPE: DNA
ORGANISM: Bacillus clausii
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ... (654)
OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Clausen, Tb Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-0-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 84881
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US-09-974-300-5531
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.6%;
Best Local Similarity 51.8%;
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                                                                                                                                                                                                                                                                                                                                         GGTCACTGGTGAAGGAAAGATAAATGGATATCCCGTTGTCATTGCAGTTTATGGACTCCA
                                                                                                                                                                   GCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCG-CGGCTGTGCAGCGTC
                                                                                                                                                                                                                                                                                                       TGGCCTCGTGGGGTTCATCTGGGCATCTTTTGCGGAACCCCGCGCGCAGATAGGTT
                                                                                                                                   GCAAGAAGGCATGCTCAGCCTTATGCAAATGGCGAAAAACGAGCGCCGCCNTTGAAGCGTC
                                                                                                 ACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCA 4,84
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Pred. No. 1.2e-19;
0; Mismatches 264;
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; NAME/KEY: CDS
; LOCATION: (1)...(891)
US-09-815-242-7115
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US-09-815-242-7115
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SEQ ID NO 7115
                                                                                                                                                                                                                                                                        Query Match 6.5%;
Best Local Similarity 49.5%;
Matches 248; Conservative
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith |
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 891
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359 CGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGC 418
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                                                                                                                CGAACTTTGCTTTTATGGGCGGTTCAATGGGTTCTGTAGTTGGTGCAAAATTTGTTAAAG
                                                                                                                                             CCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGG
                                                                                                                                                                                              AAGATGCGCTAATTACTATGACAGGTACACTTTATAATATGCCAATCGTTGTGGCTGCAT
                                                                                                                                                                                                                         ATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGT 238
                                                                           CGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCCTGCTTCCGGTGGTG 358
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                                    CGGCTGAAAAAGCGATGGAAATGAATTGTCCATTTGTGTGTTTCTCTGCGAGTGGTG
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Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
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Pred. No. 2.1e-19;
0; Mismatches 253;
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Searc	g 4	g Q	B &	망양	Db Qy	рb
Search completed: November 13, 2003, 06:16:54 Job time : 912.783 secs	659 AATTGCGTGCAGCGGTGGCAA 679 	599 TGCAGCAGGCGGAGAATTTGGTGAAAACTGGTGTGTATTGATGGAATTGTGTCGCCACTCC 658	539 TAGGITICCIGGGICCICGCGIGGIGGGGGITAACCACIGGGCAIGCGCTICCAGACGGIG 598	479 GCGCCATGGCCTCGTGGGGTTCATCTGGGCATTTTGCGGAACCCGGGCGCAGA 538	419 AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG 478	

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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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            400100
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                                                                                                           2448
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seq length: 2000000000
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Enterococcus faeca
H. pylori GHPO 451
Helicobacter pylor
Helicobacter pylor
Salmonella typhi c
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C glutamicum prote
Corynebacterium gl
Mycobacterium cube
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taphyl	AAY72365	22	314		274	
– .	ABP57631	24	526	:-	275	
Staphylococcus aur	AAU37315	22	314		275	
Staphylococcus aur	AAU34396	22	309		277	
Bativum A	AAW48309	19	875	:	282	
Staphylococcus	ABP38941	23	315		283.5	
S. coelicolor #	AAU98725	23	527		285	
Bifidobacter	ABP66186	23	540	11.7	285.5	
Hé	AAE30458	24	315		288	
H.	AAU35421	22	315		288	
Magnetospirull	AAW27453	18	317	11.8	289	
S	AAG83050	22	280	۲	91	
Streptoco	ABP28022	23	256	11.9	291.5	
Listeria	ABB48047	23	318	Ņ	8	
	AAB96609	22	527	٢	307	
Listeria	ABB48048	23	294	·	18	_
Chlamydia p	AAY34658	20	255	13.1	319.5	_
Pseudomonas as	AAU36305	22	290	ω.	29	-
S. pneu	ABU00780	24	288	13.6	334	-
CFE 67 proteir	AAM01064	22	288	ü	334	
Streptococcus	AAU38025	22	288	ω.	334	-
Streptococcus	AAU37772	22	288	·	334	
73	ABP28020	23	288	ω.	335	
taphylococcus	92	22	252	Ψ	40	
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a	2	22	285	14.0	43	_
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taphylococcus	395	23	293	4	5	_
ש	AAG83049	22	285	14.5	354.5	-
Novel human diagno	u	22	1106	4.	9	
Helicobacter pylor	097	23	279	٠.	362	-
Protein involved i	AAY36893	20	312	٠.	364	
8	801	23	291	٠.	365	-
emophilus influ	561	22	296	5	368	
ctococcus lacti	6	23	288		368	
E. coli cellular p	AAU34637	22	304	15.3	374	_

ALIGNMENTS

RESULT 1
AAB45789
ID AAB4
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AC AAB4
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AAB45789 standard;

Protein;

491 AA

AAB45789; 15-MAR-2001

(first entry)

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	N-PSDB; AAC82732, AAC82733.	WPI; 2001-042411/06.		Tilg Y, Eggeling L, Eikmanns B, Sahm H, Moeckel B;		(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.	(DEGS) DEGUSSA-HUELS AG.		27-MAY-1999; 99DE-1024365.		10-MAY-2000; 2000EP-0109842.		29-NOV-2000.		EP1055725-A2.		Corynebacterium glutamicum.		medicine; pharmaceutical industry.	L-amino acid; accDA; coryneform microorganism; L-lysine; animal feed;		C. glutamicum accDA protein.	

PT

Cloned Corynebacterium glutamicum accDA gene useful for producing

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 Coryneform bacterium; organic acid synthesis
                                                      C glutamicum
                                                                                         26-SEP-2001
                                                                                                                                                              AAG90675 standard; Protein; 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coryneform bacterium that overexpresses the accDA gene. Coryneform bacteria transformed with (I) so that they overexpress the accDA gene useful for producing L-amino acids, especially L-lysine, which are useful in animal feeds, in human medicine and in the pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transformed coryneform bacteria producing increased yields of L-amino
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                                                                                                                                                                                                                                                  SRFTRFERLAQ 491
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                                                      protein fragment SEQ ID NO: 4429.
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                    amino acid synthesis; vitamin;
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Pred. No. 7.6e-215;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. Tare useful for identifying the mutation point of a gene derived from mutation point of a gene derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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07-APR-2000;
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Senoh A, Ikeda
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Pred. No. 1.4e-214;
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AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
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ilarity 100.0%;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying nucleotide or polypeptide sequence for use as drug targe involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may useful as a target for a drug or essential for the growth or viability
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  ---TLGPQELRFARRGISLARELNLPIVSIIDTSGAELSQAAEELGIASSIARTLSKLID
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47.8%; Pred. No. 8.6e-87;
ative 73; Mismatches 153;
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23-MAY-2000;
26-MAY-2000;
                                                                                                   The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to obtain antibodies capable of binding to the express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drig discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation is a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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N-PSDB; AAS53191.
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-2000;
27-NOV-2000;
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2000US-207727P.
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2000US-257931P
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Xu HH;
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This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                               New isolated Helicobacter polynucleotides -
for the diagnosis, prevention and treatment
infections and gastrointestinal diseases
                                                                                         Claim 8; Page 738-739;
                                                                                                                                                                                                         Al-Garawi
                                                                                                                                                                                                                                                                                 29-JUL-1997;
01-APR-1997;
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peptic ulcer (
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MERIEUX ORAVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 AA;
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97US-0833457.
97US-0881227.
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42.6%;
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AX PASTEUR MERIEUX SERUMS
                                                                                        2054pp; English.
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Pred. No. 5.
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                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                              Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                          23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                            23-MAY-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                  Helicobacter pylori
                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic cellular proliferation
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DB; AAS53651.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 AA;
                                                                                                                                                                                                                                                                                                                   antibacterial;
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                                                                                                                                                                                          2000US-242578P.
2000US-253625P.
                                                                                                                                                                                                            2000US-206848P.
2000US-207727P.
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                                                                                                                               Ohlsen
Xu HH;
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..5e-26;
les 72;
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                                                                                                                                        Trawick JD,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The

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Seq ID No 11385; 511pp;

English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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     Claim 6; Page 172; 642pp; English
                                                     ulcers in mammals
                                                                           New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                   02-JAN-2001; 2001US-259302P
                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2001; 2001WO-EP,15428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein-protein interaction; ulcer; selected interacting domain;
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                                                                                                                                                                                                                                       Legrain
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                                                                                                                                                                                                                                       Rain J,
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1.5e-26;
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                                                                                      preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to represent an illegible residue.
                                                                                                                                                                                                                            27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                      21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhi.
                          N-PSDB; AAS56218
                                                 WPI; 2001-611495/70.
                                                                                                   Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001WO-US09180
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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                                                                                                   Ohlsen
Xu HH;
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41.2%; Pre
ative 37;
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Pred. No. 1.3e-26;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
 21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                        21-MAR-2001;
                                                                                                                           27-SEP-2001
                                                                                                                                                             WO200170955-A2
                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                 Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                        14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                           AAU34637;
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                                                                                                                                                                                                                                                                                                                                                                                            AAU34637 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                   coli cellular proliferation protein #218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAALAKMOERGLPYISVLTDPTMGGVSASFAMLGDLNIAEPKALIGFAGPRVIEQTVREK
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 ; 2000US-191078P.
; 2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
                                                                                                                                                                                                                               antibacterial; drug
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                                                                                        2001WO-US09180
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Pred. No. 1.2e-25;
9; Mismatches 92;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form of the printed specification, but was obtained in eleformat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
                                Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                      ABB54092 standard; Protein; 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Lactococcus lactis IL1403
                                                                  Lactococcus lactis protein accD
                                                                                                      16-MAY-2002
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Yamamoto RT,
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22-DEC-2000; 2000US-257931P
16-FEB-2001; 2001US-269308P
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                                                                                                                                                                                                                                                                                                                                                                                               121 VAAAFEFAFMGGSMGSVVGARFVRAVEQALEDNCPLICFSASGGARMQEALMSLMQMAKT 180
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                                                                                                                                                                                                                                                                                                                                                             TAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHA 195
                                                                                                                                                                                                                                                                                                                                                                                                                   AVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSI 135
                                                                                                                                                                                                                                                                                         LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP 251
                                                                                                                                                                                                                                                                                                                             SAALAKMOERGIPYISVLTDPTMGGVSASFAMLGDLNIAEPKALIGFAGPRVIEQTVREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SÍVELGSELEPKDVLKFRDSKKYKÓRLASAQKÉTGÉK-----DALVVMKGTLYGMPV
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                                                                                                                                                                                                                                                         LPPGFQRSEFLIEKGAIDMIVRRPEMRLKLASILAKLMNLPAPNPEAP-REGVVVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 374; DB
Pred. No. 1.3e
49; Mismatches
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1.3e-25;
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RESULT 12
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Best Local S
Matches 86
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 27-SEP-2001
                          WO200170955-A2
                                                                           Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
                                                                                                                 Haemophilus influenzae cellular proliferation protein #260.
                                                                                                                                             14-FEB-2002
                                                                                                                                                                       AAU35619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleotide sequence useful in
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                                                                                                                                                                                                 AAU35619 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                         QAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVE
                                                                                                                                                                                                                                                                                                                   HSNAGLFYITVLTDPTTGGVTASFASLGDIILAEPQSLIGFAGRRVIEQTVRQTLPDDFQ
                                                                                                                                                                                                                                                                                                                                                                       STFIMASMGTVVGEKLTRLFEYATTEKLPIIVFTASGGARMQEGIMSLMQMAKTSAAVKR
                                                                                                                                                                                                                                                                                                                                                                                                                           VADKDSFVEMFTGIESKNPLDFPGYPEKLAATKARTGLDEAVITGTATIKGQKTALAIMD
                                                                                                                                                                                                                                                                                                                                             HREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQ
                                                                                                                                                                                                                                                                                                                                                                                                FSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID No 794;
                                                                                                                                                                                                                                                                  KAEFLLNHGFVDAIVKRTELRQKLALLLELHTEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLDPDSFISWNETPQYDN-LN-QGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSD
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                                                  influenzae
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                                                                                                                                                                                                Protein;
                                                                                                                                             entry)
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40.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 368; DB 23;
Pred. No. 4.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the identification or Lactococcus
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ABP28019
ID ABP2
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AC ABP2
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ABP28019 standard;

Protein; 291

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ABP28019;

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Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The pneumoniae is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent this data for the present sequence is also useful to screen compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essentigenes themselves and the encoded proteins. The prokaryotes used are
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                               of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-611495/70.
DB; AAS53478.
                                                              191
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251
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                                                                                                                                                                                                                                                     81;
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Seq ID No 11212; 511pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELITRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT,
                                                                                                                                                                                                               LDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFS
                           ENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSP 243
                                                              EKGVPFISVLTDPTLGGVSÅSFAMLGDLNIÅEPKALIGFÄGPRVIEQTVREKLPEGFQRS
                                                                                           EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQA
                                                                                                                          FMGGSMGSVVGAKFVKAAEKAMEMNCPFVCFSASGGARMQEALFSLMQMAKTSAVLAQMR
                                                                                                                                                        FLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHR 143
                                                                                                                                                                                       LEPKDILKFKDLKKYKDRINAAQKETGEK-----DALITMTGTLYNMPIVVAASNFA
                                                                                                                                                                                                                                                                                                                   296 AA;
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2000US-257931P.
2001US-269308P.
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2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                                                                                                                                                     Conservative
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHARM INC
                                                                                                                                                                                                                                                                  15.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences of antisense nucleic
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                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                                                 Score 368; DB 22,
Pred. No. 4.6e-25;
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02-JUL-2002

(first

entry)

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253

QKAEFLLEHGFVDAIINRTELRDCIAQLI 281

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Query Match
                                                                                                                                                                                                                                                                                                                                                           Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds t (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated me meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus/GBS agalactiae) or group A streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71556 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 3685; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for detecting a compound that binds to the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR-)
                                                                                                                                                                                                                                                                   Local
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INST GE
                                                                                                                                                                                                                                                                 Similarity
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QQAENLVKTGVIDGIVSPLQLRAAVAKTL
|:|| |:: | || :| :|: :|
                                                                                                                                        DFSFLGGSLGTVASVRIMKAIHRATBLKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQ
                                                                                                                                                                              VDEDSFEELFTGIETK--DPLNFPNYREKLAATROKTNIDEAVVTGLAKIKGOTTALAIM
                                                                                                                                                                                                RHSNQGLFYLTILTDPTTGGVTASFAMEGDIILAEPQALVGFAGRRVIETTVREDLPEGF
                                                                               RHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGV
                                                                                                                DSHFIMASMGTVVGEKLTRLFELATEKKLPIVIFTASGGARMQEGIMSLMQMAKVSAAVK
                                                                                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masignani V,
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                                                                                                                                                                                                                                                                                                                                                   proteins.
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                                                                                                                                                                                                                                                                14.9%;
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                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                              Score 365; DB 23;
Pred. No. 8.4e-25;
8; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                      AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma and invitation.
                                                                                                                                                                                                                                                                                                                                paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 761; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-371125/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-1998;
28-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY36893 standard; Protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bartholinitis; pneumopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      paratrachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY36893;
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                                                                                                                                                                                                                                               Local
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 253
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                                                                                                                                                                                                                                   81;
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    involved in intermediate metabolism
EFLLEHGMIDKVVERKQLKTTLESLL
                           ENLVKTGVIDGIVSPLQLRAAVAKTL 229
                                                        EAKLPYISVLTNPTSGGVTASFASLGDVIIAEPKALICFAGPRVVSQVIGEDLPEGAOKS
                                                                                  EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQA 203
                                                                                                                                          FLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHR 143
                                                                                                                                                                         SWNPLFSDLRSQDPLNFVDTDTYPNRLEKARKDNPDSEGVLVGACTIGSYPVALAVMDFS
                                                                                                                                                                                                    SWN----ETPOYDNLN----QGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFS
                                                                                                               FMAGSMGAVVGEKLTRLIEKAIDSRLPVIIVSASGGARMQESVFSLMQMAKTSAALAKLH
                                                                                                                                                                                                                                                                                                                        use
                                                                                                                                                                                                                                                                                            312 AA;
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                      in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inclusion conjunctivitis; genital
uretritis; epidymitis; cervicitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                                                             14.9%;
                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                Score 364; DB 20;
Pred. No. 1.2e-24;
35; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervicitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease; perihepatitis;
                                                                                                                                                                                                                                                            Length 312;
                                                                                                                                                                                                                                 Indels
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RESULT 15
ABU50977
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Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori selected interacting domain (SID) protein #320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing ulcers in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-674910/72.
N-PSDB; ABX65721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein-protein interaction; ulcer; selected interacting domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU50977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU50977 standard; Protein; 279 AA.
                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JAN-2001; 2001US-259302P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2001; 2001WO-EP15428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                       identified via protein-protein interactions.

Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to represent an illegible residue.
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 164; 642pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Legrain P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYBR-) HYBRIGENICS.
(INSP ) INST PASTEUR.
   234
                                 195
                                                               174
                                                                                                                         115 LQ-IWFDFSFMGGSLGSVEXEKIVRAINRAVAKREALLIVSASGGARMQESTYSLMQMAK 173
                                                                                            135
                                                                                                                                                                                      56
                                                                                                                                                      75
                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                  , 68
                                                                                                                                                                                                                                                               Similarity
                                                              TSAALNRLSEAKLÞFISLLSDÞTYGGVSASFAFLGDLIIÁBÞGAMÍGFAGÞRVIKQTIGA
DLPEGFOTAEFILEHGLIDMÍVHRKDÍKKTLSDLIAMMTHKTSKI 278
                       ALPDGVQQAENLVKTGVIDGIVSPLQLRAAVA------KTLKV 231
                                                                                           ITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGH 194
                                                                                                                                              VAVILSDESELGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMVVS 134
                                                                                                                                                                                    IEFLCDVGSFEEFDKHLRPN-DPLNXVDKESYKQRIKKYEKRTNRPSSVISGXAKINRMP
                                                                                                                                                                                                               IDSVLDPDSFISWNE---TPQYDNLN----QGYAETLERARSKAKCDESVITGEGTVEGIP 74
                                                                                                                                                                                                                                                                                                             279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rain J,
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                               14.8%; Score 362; DB 23; 39.6%; Pred. No. 1.5e-24; tive 40; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colland F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Reuse H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Labigne A;
                                                                                                                                                                                                                                                                               Length 279;
                                                                                                                                                                                                                                                    Indels 16;
                                                                                                                                                                                                                                                    Gaps
                                                                    233
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Search completed: November 13, 2003, 06:40:21 Job time .: 80 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   431.5
392.5
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Match Length
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2448
1 VEKREPTMVWGMEHTSALTL......NNPERAGRDSRETREERLAQ 491
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283308 seqs, 96168682 residues
                                                                       Copyright
   GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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                  E70784
AE2101
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1242.601 Million cell updates/sec
              acetyl-coenzyme A acetyl-CoA carboxy probable acctyl-CoA carboxy probable acctyl-CoA carboxy probable acetyl-CoA carboxy probable
                                                                                                                                                                                                                                                                                                                                                                                                                                      acetyl-CoA carboxy acetyl-coenzyme A
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acetyl-CoA carboxy
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protein
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
323.5	326.5	327	329	329.5	330.5	330.5	331.5	331.5	332	332.5	334	334	334	336	343.5
13.2	13.3	13.4	13.4	13.5	13.5	13.5	13.5	13.5	13.6	13.6	13.6	13.6	13.6	13.7	14.0
493	512	516	288	290	515	294	507	489	307	432	308	288	288	285	285
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
S78384	A05196	A69527	S73119	C83257	C72344	AG1633	T07012	S66564	D87688	T06341	882253	в97920	D95049	A97338	A89954
acetyl-CoA carboxy	hypothetical prote	methylmalonyl-CoA	acetyl-CoA carboxy	acetyl-CoA carboxy	propionyl-CoA carb	acetyl-CoA carboxy	acetyl-CoA carboxy	acetyl CoA carboxy	hypothetical prote	acetyl-CoA carboxy	acetyl-CoA carboxy	acetyl-CoA carboxy		acetyl-CoA carboxy	acetyl-CoA carboxy

ALIGNMENTS

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Qy 372 APLPTVSVIIGQGVGGGGALAMLPADLVYAAENAWLSALPPEGASAILFRDTNHAAEIIER	Qy 315TLGPQELRFARRGISLARELNLPIVSIIDTSGAELSQAAEELGIASSIARTLSKLID	Qy 257 ARSRDPQRPGIGEIMETLGADVVKLSGARAGALSPAVRVALARIGGRPVVLIGQDRRF	Qy 203 AENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALPVMEAI : : : :	Qy 143 REAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQ	Oy 83 SFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRH 142	Qy 23 SVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDF	Query Match 42.8%; Score 1047; DB 2; Length 495; Best Local Similarity 47.8%; Pred. No. 1.2e-57; Matches 233; Conservative 73; Mismatches 153; Indels 28; Gaps	RESULT 1 PROBABLE accD3 protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-U1-1998 #sequence_revision 17-U1-1998 #text_change 20-Jun-2000 C;Accession: E70783 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genor A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: E70783 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-495 <col/> A;Experimental source: strain H37Rv C;Genetics: A;Gene: accD3 C;Superfamily: propionyl-CoA carboxylase beta chain
R 431	D 371 T 365	- 314 G 305	I 256 : V 246	Q 202 T 191	H 142 H 131	F 82 F 71	8 ,	7RV) e 20-Jun-2000 C.; Harris, D.; Gordon, S.; Hamlin, N.; Holroyd, S.S.; Squares, S. s.; Barrell, B.G. from the complete genome ation not shown :CAA97379.1; PID:g1314044

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AF3504
acetyl-CoA carboxylase (EC 6.4.1.2) [imported] - Brucella melitensis (strain C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C;Accession: AF3504
C;Accession: AF3504
C;Accession: AF3504
                                                                                                                                                                                                                                                                                                                 RESULT 3
AE2101
                                                                              R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Wata Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yas DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2101
                                                                                                                                                                                                                          acetyl-CoA carboxylase beta chain [imported] - Nostoc sp. (strai C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
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A;Map position: I
C;Superfamily: acetyl-CoA
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: AD3252; PMID:11756688
A;Accession: AF3504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-301 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL53201.1;
A;Cross-references: GB:BA000019; PIDN:BAB74063.1; PID:g17131456; GSPDB:GN00179
                   A;Residues:
                                  A; Molecule type: DNA
                                                             A; Status: preliminary
                                                                                                                                                                                                        C;Accession: AE2101
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Best Local :
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                   1-316 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGVQAHALLSQGLIDGIVAETEHFVEEILG---TISNALSELDN-----NPERAGRDSR 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELKRPLVLFASSGGARMQEGILSLMQLPRTTVAVEMLKEAGLPYIVVLTNPTTGGVTASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASW 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                AKTLKVI - - QPVEATDRFSPTTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMLGDIHIAEPGALIGFAGPRVIEQTIREKLPEGFQSSEYLMEHGMVDMVVSRLELKATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 431.5;
Pred. No. 1e-1
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      294
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                                                                                                                                                                                                                                                                                                (strain PCC 7120)
                                                                                                                                                                 S.; Watanabe, A.; M.; Yasuda, M.; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain
                                                                                                                                                                                                                                strain PCC 7120
09-Dec-2002
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RESULT 5
F64638
acetyl-CoA
C;Species:

carboxylase beta subunit Helicobacter pylori

Helicobacter

pylori (strain

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acetyl-coenzyme A carboxylase chain B - Helicobacter pylori (strain J99)
c(species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Jul-1999
C;Accession: E71875
C;Accession: E71875
F;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; 7
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: E71875
A;Accession: E71875
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE001518; GB:AE001439; NID:g4155454; PIDN:AAD06468.1; PID:g415546: A;Experimental source: strain J99 C;Genetics: A;Gene accD A;Gene: accD C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase beta chain
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E71875
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                                                                                        179 MOMAKTSAALNRLSEAKLÞFISLLSDÞTYGGVSÁSFAFLGDLIIÁEÞGAMÍGFAGÞRVIK 238
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                                                                                                                                                                                                                            70
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87; Conserv
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                                                                                                                                                                                                                     VEGIPVAVILSDESFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAF 129
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                                LTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVA-----KTLKV 231
                                                                                                                                 VMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVE 189
QTIGADLPEGFQTAEFLLEHGLIDMIVHRKDLKKTLSDLIAMMTHKTSKI
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Pred. No. 2.8e-17;
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C; Superfamily: a
C; Keywords: liga
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AD0802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AD0802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acetyl-CoA carboxylase (EC 6.4.1.2) - Salmonella enterica subsp. enterica serovar C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi
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A;Molecule type: DNA
A;Residues: 1-289 <TOM>
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A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64638
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                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
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A; Residues: 1-304 < PAR>
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C; Accession: F64638
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                                                                                                                                                                                                                                                                                 Superfamily: acetyl-CoA carboxylase, Keywords: ligase
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VAAAFEFAFMGGSMGSVVGARFVRAVEQALEDNCPLVCFSASGGARMQEALMSLMQMAKT
                                        AVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSI 135
                                                                                                                                       ALTLIDSVLDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPV
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                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                              GB:AL513382; PIDN:CAD07598.1; PID:g16503590; GSPDB:GN00176
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                                                                                                                                                                                                                Score 375; DB 2;
Pred. No. 3.3e-16;
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Pred. No. 8
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                                                                                                                LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP
                                                                                                                                                                                             TAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHA 195
                                                                                                                                                        SAALAKMQERGLPYISVLTDPTMGGVSASFAMLGDLNIAEPKALIGFAGPRVIEQTVREK 240
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia A;Reference number: A64720; MUID:97426617; PMID:92785 A;Accession: B65004 C;Date: 31-Dec-1988 #sequence revision 05-Dec-1997 #text_change 01-Mar-2002 C;Accession: B65004; C29803; B29805; E40637; I41212 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; A; Rose, D.J.; Mau, B.; Shao, Y. acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase N,Contains: carboxyltransferase beta chain A;Cross-references: GB:AE000320; A; Molecule type: DNA A;Status: nucleic acid sequence not shown; translation not A;Residues: 1-304 <BLAT> ;Species: Escherichia coli GB:U00096; NID:g1788647; 12, substrain MG1655 PMID: 9278503 coli beta PIDN:AAC75376.1; PID:g1788655 K-12 chain [validated] V.; Riley, Identification **3** Escher ဂ္ဂ

J. Biol. Chem. 262, 12209-12217, 1987
A; Title: The hisT-purf region of the Escherichia coli K-12
A; Reference number: A29803; MUID:87308226; PMID:3040734 A; Experimental source: strain K-12, substrain R; Nonet, M.L.; Marvel, C.C.; Tolan, D.R. A; Accession: C29803

A; Rolecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-75, 'SV', 78-225, 'ALPVRVLSNR', 236-304 <NON>
A; Residues: GB: M68934; GB: J02800; NID: g146359; PIDN: AAA23965.1; PID: 9146364

A;Experimental source: strain K12
R;Bognar, A.L.; Osborne, C.; Shane, B.
J. Biol. Chem. 262, 12337-12343, 1987
A;Title: Primary structure of the Escherichia coli folc A;Reference number: A29805; MUID:87308246; PMID:3040739
A;Accession: B29805 gene and 118 folylpolyglutamate

<BOG>
PIDN:AAA23807.1;

PID: g146019

A; Molecule type: DNA
A; Residues: 1-224, 'MALPVRVLSNRPFAK', 240-304
A; Cross-references: GB: M32445; NID: g146018;
R; Li, S.J.; Cronan Jr., J.E.

J. Bacteriol. 175, 332-340, 1993
A;Title: Growth rate regulation of Escherichia coli acetyl A;Reference number: A40637, MUID:93123150; PMID:7678242
A;Accession: E40637 coenzyme A carboxylase, which

A; Molecule type: DNA A; Residues: 1-32 <LI1> A;Status: preliminary

A;Cross-references: GB:S53037; NID:g263402; PIDN:AAB24894.1; A;Note: sequence extracted from NCBI backbone (NCBIN:122320, R;Bogner, A.L.; Osborne, C.; Shane, B J. Biol. Chem. 262, 12334-12343, 1987 PID: 9263404 NCBIP: 122322

J. Biol. Chem. 262, 12334-12343, 1707, A;Title: Primary structure of the Escherichia coli A;Reference number: I41212
A;Accession: I41212

folc

gene

and its folylpolyglutamate

A; Status: translated from

A; Molecule type: DNA A;Residues: 1-224, 'MALPVRVLSNRPFAK', 240-304 A;Residues: GB:J02808; NID:9148007; <RES>
PIDN:AAA23801.1; PID: 9146008

A;Gene: accD; dedB; usg

A; Map position: 50 min C; Complex: in E. coli, otin carboxyl carrier protein <ACC> acetyl-CoA carboxylase is
protein (BCCP, homodimer) composed of biotin carboxylase
(PIR:BKEC9) (EC 6 .3

A; Description: EC 6.4.1.2 [validated, MUID:75035569]; the acetyl-COA carboxylase

A;Pathway: fatty acid biosynthesis C;Function: <CTRB> A;Description: catalyzes the transfer of the carboxyl group from the carboxyl-biotin

complex

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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasr iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia cc A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85873
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acetyl-CoA carboxylase C;Species: Escherichia C;Date: 18-Jul-2001 #se
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A;Experimental source: strain O157:H7, substrain EDL933
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A; Residues: 1-304 <STO>
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Best Local
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  #sequence_revision 18-Jul-2001
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; Pred. No. 3.8e-16;
49; Mismatches 92
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                                                carboxyltransferase beta chain [similarity]
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  #text_change 31-Dec-2001
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LHGLPVTLAVMDFAFSGGSMGSVVGEEIARAAEYAAESRTPLLLVAASGGARMQESALSL

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A;Status: A:Constant A;Nolecule type: DNA
A;Residues: 1-284 <WHI>
A;Cross-references: GB:AE001970;
A;Cross-imantal source: strain R1
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
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A; Residues: 1-304 <HAY>
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C;Accession: A75422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLVELGSELEPKDVLKFRDSKKYKDRLASAQKETGEK------DALVVMKGTLYGMPV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTLIDSVLDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPV 75
                                               SAERRVEVLADPGSFRQLSGQVHP-VDPLHFTDTEPYPERLRRAQAKTGRPDAILTGTAT
                                                                                       SALTLIDSVLDPDSF--ISWNETPQYDNLN----QGYAETLERARSKAKCDESVITGEGT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii,
Kasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                Conservative
                                                                                                                                               15.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carboxylase,
                                                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                    GB:AE000513; NID:g6458956; PIDN:AAF10788.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 374; DB 2; 1
Pred. No. 3.8e-16;
l9; Mismatches 92;
                                                                                                                                                   Score 372.5;
Pred. No. 4.1
                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carboxyltransferase beta
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                                                                                                                                4.3e-16;
ches 90;
                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change 17-Mar-2000
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M.; Shinagawa,
                                                                                                                                                                           284;
                                                                                                                                                                                                                 chain
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                                                                                                                                7;
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                                                   114
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A; PROJECTION OF A PROPOSITION OF A PROPOSITION OF A; Cross-references: GB: AE000690; NID: g2983100; AE000690; AE000
                                                                                                 A;Experimental source: strain C;Genetics: C;Genetics: A;Gene: accD A;Gene: accD C;Superfamily: acetyl-CoA carb
                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete genome of the hyperthermophilic b. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: F70340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acetyl-CoA carboxyltransferase beta subunit - Aquifex aeolicus C;Species: Aquifex aeolicus C;Decies: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change C;Accession: F70340
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                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઇ
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   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.; Warren, P.V.; Gaasterland,
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   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQMAKTTVALEALSGRGVPYLSLLTDPTTGGVTASFATIADVIIAEPGALIGFAGPRVIC
                                                                                                 acetyl-CoA carboxylase, carboxyltransferase
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15.1%;
38.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%; Score 370.5; DB 2
36.5%; Pred. No. 5.7e-16;
   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta subunit accD [imported] - Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                      sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
369.5; DB 2;
No. 6.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T.; Young,
                                                                                                                                                                                                                                                                                                                                      not
                                                                                                                                                                                                                              PIDN:AAC06712.1; PID:g2983107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                      shown; translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterium Aquifex aeolicus
                                  Length 276;
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                                                                                                 beta chain
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RESULT 13
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                                                                                                                                                                                                                                              Similarity
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                      QAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVE
                                                                                HREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQ
                                                                                                              STFIMASMGTVVGEKLTRLFEYATTEKLPIIVFTASGGARMQEGIMSLMQMAKTSAAVKR
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                                                   HSNAGLFYITVLTDPTTGGVTASFASLGDIILAEPQSLIGFAGRRVIEQTVRQTLPDDFQ
                                                                                                                                         FSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQR
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40.0%;
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                                                                                                                                                                                                                             Score 368; DB 2;
Pred. No. 8.4e-16;
7; Mismatches 90
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acetyl-CoA carboxylase (BC 6.4.1.2) carboxyltransferase beta chain - Haemophilus influe C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Date: 18 - Aug-1995 # sequence_revision 23-Feb-1996 # text_change 18-Jun-1999
C; Accession: B64113
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Reference number: A64000; MUID:95350630; PMID:7542800

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B64113

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A;Description: the enzyme complex catalyzes the synthesis of malonyl-CoA; the tin bound to BCCP (see BKEC9) with bicarbonate; carboxyltransferase catalyzes A;Pathway: fatty acid biosynthesis A;Note: first committed step C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase beta chain C;Keywords: fatty acid biosynthesis; ligase; zinc finger F;29-51/Region: zinc finger CCCC motif
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A;Residues: 1-296 <TIGR>
A;Cross-references: GB:U32806; GB:L42023; NID:g1574717; PIDN:AAC22913.1; PID:g1574718;
A;Note: named as homolog to a protein from Escherichia coli
C;Function:
                                                                                                                                                                                                                                                                                                                                                                        R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler A;Authors: Foulger, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel A;M.; Ogawa, K.; Ogiwara, A. J. Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Y; M.; Ogawa, K.; Ogiwara, A. J. Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Y; M.; Ogawa, K.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron A; Mithers, P.; Mipat, A.; Tanaka, T.; Trepstra, P.; Tognoni, A.; Togato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Zamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Althors: Yoshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A,Rocaesia, Conon
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C;Species: Bacillus subtilis
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                                                                                                              A;Gene: yttI
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase beta chain
                                                                                                                                                                                                       A;Residues: 1-262 <KUN>
A;Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14881.1; PID:g2635386
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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84;
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                            14.8%; Score 363; DB 2; 38.2%; Pred. No. 1.5e-15;
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   41; Mismatches
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                                                                                                                              GVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEAT 238
                                         lklfseeqgliisvmthþttggvsasfaslgdynfaeþgaligfagrkiieqtigeklþe
                                                            VQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFABPGAQTGFLGPRVVBLTTGHALPD 198
                                                                                    DFQTAEFLLKHGQLDAVIH----RDDMKKTLENLLDMHQT
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Search completed: November 13, 2003, 06:45:04 Job time : 39 secs

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Result
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1 saccharopol
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4 salmonella
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4 sus scrofa
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6 secherickia
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	_		Q06101 rhodococcus		_		P96885 mycobacteri	Q54766 synechococc		025283 helicobacte		P74638 synechocyst

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RESULT 1

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ID ACCD_MYCTU STANDARD; PRT; 495 AA.

AC Q10561;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative acetyl-coenzyme A carboxylase carboxyl transferase subunit
DE beta (EC 6.4.1.2) (ACCASE beta chain).
ACCD3 OR RV0904C OR MT0927 OR MTCY31.32C.

OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

NCBI TaxID=1773;
RN [1]

modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@ib-sib.ch).	នននន
This SWISS-PROT entry is copyright. It is produced through the swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contermants.	18888
THE ACCEPTAGE TO THE AC	388
+ malonyl-CoA.	38
-!- CATALYTIC ACTIVITY: 1	88
CARBOXYLA	188
-!- FUNCTION: THIS PROTEIN IS A	38
laboratory strains."; Submitted (APR-2001) to the EMRI/GenBank/DDRT databases	R RI
"Whole	RT
Delcher A., Utterback T., Wej Bishai W.;	RA RA
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg	R 3
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STRAIN=CDC 1551 / Oshkosh;	RC RC
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Rutter S., Seeger K., Skelton S., i	R R
Oliver S., Osborne J., Quail M.A., Rajandream M.A., R	R.A
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,	₽:
Davies R. Devlin K. Feltwell T	R R
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,	₽₽
Cole S.T., Brosch R., Parkhill J.,	₽.
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S Mycobacterium tuberculosis.	ပ္ပ
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Putative acetyl-coenzyme A	멾
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Matches 233
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InterPro; IPR0000438; ACOACC transfB.
InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
Hypothetical protein; Fatty acid biosynthesis; Ligase;
Complete proteome.
SEQUENCE 495 AA; 51772 MW; 156C96E927FF950C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z73101; CAA973
EMBL; AE006979; AAK4
PIR; E70783; E70783.
                                                                                                                                                                                                                                                                       ACCD SYNP7 STANDARD; PRT; 305 AA. 054776; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Acetyl-coenzyme A carboxylase caraboxyl transferase (EC 6.4.1.2) (ACCASE beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR; MT0927;
     Phung L.T., Haselkorn R.;
Submitted (JUL-1996) To the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1996) TO THE ACETYL COENS
SUBMITTED THE ACETYL COENS
CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES
                                                                                                                                                                 Synechococcus sp. (strain PCC 7942) (Anacystis nidular Bacteria; Cyanobacteria; Chroococcales; Synechococcus NCBI_TaxID=1140;
                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOARLÞYLVYLRHÞTTGGVFÁSWGSLGHLTVÁEÞGÁLIGÞRÚYELLYGDÞFÞSGVOT
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Pred. No. 1.1e-54;
3; Mismatches 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                     FACCD_ECOLI STANDARD; PRT; 304 AA.

P08193; P76937; P78251;

01-AUG-1988 (Rel. 08, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Acetyl-coenzyme A carboxylse carboxyl transferase

(EC 6.4.1.2) (ACCase beta chain).

ACCD GR DEDB OR USG OR B2316 OR Z3578 OR ECS3200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRPAMS; TIGR00515; accD; 1.
Fatty acid biosynthesis; Ligase; Zinc-finger.
ZN_FING 33 55 C4-TYPE (POTENTIAL)
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TIGRFAMS; TIGR00515; accD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000438; ACoACC_transfB
InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U59237; AAB82034.1;
                                                                                         Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334;
SEQUENCE FROM N.A.
MEDLINE=87308246; PubMed=3040739;
MEDLINE=87308246; PubMed=3040739;
Bognar A.L., Osborne C., Shane B.;
"Primary structure of the Escherichia coli f
folylpolyglutamate synthetase-dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + malonyl-coa.
SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUN OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY).
SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192
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Pred. No. 3.
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        synthetase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87308226; PubMed=3040734;
Nonet M.L., Marvel C.C., Tolan D.R.;
Nonet hisT-purF region of the Escherichia coli K-12 chromosome.
Identification of additional genes of the hisT and purF operons.";
J. Biol. Chem. 262:12209-12217(1987).
                                                                                                               MEDLINE=91360091;
Nagano Y., Matsuno
                                                                                                                                                                       SIMILARITY TO
                                                                                                                                                                                                                                                                                                                                       MEDLINE=93123150;
Li S.J., Cronan J.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T. Iida T., Takami H., Honda T., Salara C., Ogasawara N., Yasunag Tida T., Takami H., Hattori M., Shinagawa H.; Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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Mau B., Shao Y.,
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Blattner F.R., Plunkett G. III, Bloch C.A
Riley M., Collado-Vides J., Glasner J.D.,
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                                                                                                                                                                                                                          Bacteriol. 175:332-340(1993)
                             ano Y., Matsuno R., Sasaki Y.;
essential gene of Escherichia coli tha
a chloroplast gene of unknown function.
. Gen. Genet. 228:62-64(1991).
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                                                                                                                                                                       ZFPA.
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.E. Jr.;
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Best Local S
Matches 85
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"The dedB (usg) open reading frame of Escherichia coli encodes a subunit of acetyl-coenzyme A carboxylase.";

J. Bacteriol. 174:5755-5757(1992).

-i- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CAPALYZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSCARBOXYLASE CAPALYZES THE CARBOXYLAGE CAPALYZES THE CARBOXYLAGE.

-i- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate - mallonyl-CoA.
                                                                                                                                                                                                                                                                                          CONFLICT
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InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
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EMBL; J02808; AAA23801.1; -.
EMBL; M68934; AAA23965.1; -.
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J; D90862; BAA16165.1; -.

L; D90863; BAA16173.1; -.

L; AE005463; AAG57445.1; -.

JL; AP002561; BAB36623.1; -.

JL; AP002561; BAB36623.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUL OF CARBOXYL TRANSFERBASE IN A 2:2 COMPLEX.
SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
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                                                                                                               VAAAFEFAFMGGSMGSVVGARFVRAVEQALEDNCPLICFSASGGARMQEALMSLMQMAKT
                                                                                                                              AVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSI 135
LPPGFQRSEFLIEKGAIDMIVRRPEMRLKLASILAKLMNLPAPNPEAP-REGVVVP
                        <u>LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP</u>
                                                        SAALAKMQERGLPYISVLTDPTMGGVSASFAMLGDLNIAEPKALIGFAGPRVIEQTVREK
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                                                                                                                                                                                                                                                                                                                    ase; Zinc-finger; Complete proteome.
C4-TYPE (POTENTIAL).
EL -> SV (IN REF. 2).
IGFAGPPVIEQTVRE -> MALPVRVLSNRPFAK (IN REF. 1).
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Pred. No. 2.3e-15;
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MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougharty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Wenter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit (EC 6.4.1.2) (ACCASE beta chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                         Fatty acid
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000438; ACOACC transfB
InterPro; IPR000022; Carboxyl_trans
Pfam; PF01039; Carboxyl_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32806; AAC22913.1; -. PIR; B64113; B64113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gan
Pasteurellaceae; Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCD OR HI1260
                                                                                                                                                                                                                                                                                                        PRINTS; PR01070; ACCCTRFRASEB.
TIGRFAMs; TIGR00515; accD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + acetyl-Coa + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY). SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAEIN
   144
                                      131
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                                                                        84
                                                                                                           79
                                                                                                                                              25
                                                                                                                                                                                  81;
                                                                                                                                                                                                  Similarity
   EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQA
                                                                      FLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHR
                                                                                                                                              LDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFS
                                      FMGGSMGSVVGAKFVKAAEKAMEMNCPFVCFSASGGARMQEALFSLMQMAKTSAVLAQMR
                                                                                                           LEPKDILKFKDLKKYKDRINAAOKETGEK---
                                                                                                                                                                                                                                                                       biosynthesis; Ligase; Zinc-finger; Complete proteome 29 51 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                        296 AA;
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                        32635 MW;
                                                                                                                                                                                                15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gammaproteobacteria;
                                                                                                                                                                                  45;
                                                                                                                                                                                                  Score 368; DB 1;
Pred. No. 5.1e-15;
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                                                                                                                                                                                  Mismatches
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                                                                                                             ----DALITMTGTLYNMPIVVAASNFA
                                                                                                                                                                                  ; 08
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                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                     296;
                                                                                                                                                                                  14;
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RESULT 5
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                                                                                                                                                                                  Matches
                                                                                                                                                                                               Query Match
Best Local
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Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
Tnamura A., Yoshinaga K., Sugiura M.;
"Complete nucleotide sequence of the chloroplast genome from the
green alga Chlorolla vulgaris: the existence of genes possibly
involved in chloroplast division.";
Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
-i- FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT CARBOXYLASE
INVOLVED IN CHLOROPLAST CARBON METABOLISM.
-i- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Acetyl-coenzyme A carboxylase carboxyl transferase (EC 6.4.1.2) (ACCASE beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCD_CHLVU
P56293;
                                                                                                                                                                                                                                                                                              Pfam; PF01039; Carboxyl trans; PRINTS; PR01070; ACCCTRFRASEB. TIGR00515; accD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlorella vulgaris.
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                               Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast ZN_FING 36 58 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000438; ACOACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB001684; BAA57908.1; -. PIR; T07261; T07261.
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STRAIN=IAM C-27 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3077;
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                                                  125
                                                                                                                                                                                  102;
                                                                                 71
                                                                                                                 65
                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malonyl-CoA
                                                                                                                                                                                                 Similarity
MMVSITAAVQRHRE-AHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFILEKGAIDMIVKRSEMROTLASVIS----KLTNQPSP
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                                                                                 EGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFV 130
                                                                                                                 SSTERIESLVDANTWRPFDEMVSPCDPLEFRDQKAYTERLKDAQERTGLQDAVQTGTGLL 124
                                                                                                                                              SALTLIDSVLDPDSFISWNE----TPQYDNLNQGYAETLERARSKAKCDESVITGEGTV 70
                                                                                                                                                                                                                                                  411
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD,
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                                                                                                                                                                                                                                                46547 MW;
                                                                                                                                                                                               14.7%;
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                                                                                                                                                                                  60;
                                                                                                                                                                                             Score 361;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                  Mismatches
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.9e-14;
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                                                                                                                                                                                                              Length 411;
                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                  46;
                                                                                                                                                                                  Gaps
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RESULT
ACCD_SY
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase
(BC 6.4.1.2) (ACCASE beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNY3
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=92118327; PubMed=1368738;
Contra Y., Yoshida T., Nakamura Y., Tak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCD_SY
Q57417;
                                                                                               EMBL; D10004; BAA00893.1; -.
EMBL; S77740; AAC60398.1; -.
EMBL; D63999; BAA10092.1; -.
PIR; JQ1238; JQ1238.
   Fatty acid biosynthesis;
                                PRINTS; PR01070; ACCCTRFRASEB.
                                               InterPro; IPR000438; ACoACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synachocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T.,
Sugiura M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96127529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agric. Biol. Chem. 55:2259-2264(1991).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                       + malonyl-coa.

SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS
OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY).

SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSCARBOXYLAGED TO FORM MALONYL-COA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) =
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                  TIGR00515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8590279;
Ligase;
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Zinc-finger; Complete proteome
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protein ir
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n Synechocystis
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SEQUENCE
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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SEQUENCE
            Fatty acid biosynthesis; Ligase; Zinc-finger; Cl
ZN_FING 169 191 C4-TYPE (POTENTIAL)
                                                 InterPro; IPR000438; ACOACC_transfB
InterPro; IPR000022; Carboxyl trans
Pfam; PF01039; Carboxyl trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
                                                                                                         EMBL; U26948; AAA80643.1; -. PIR; T06341; T06341.
                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                               entities requires a
                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Resnik; TISSUE=Leaf; Reverdatto S.V., Beilinson V., Nielsen N.C. "The rps16, accb, psa1, ORF 203, ORF 151, gene cluster in the chloroplast genome of (In) Plant Gene Register PGR95-051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max (Soybean).
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01-FEB-1996 (Rel.
16-OCT-2001 (Rel.
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                                       TIGRFAMs;
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                                       TIGR00515; accD;
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33, Last sequence update)
40, Last annotation updat
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48857 MW;
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Pred. No. 1.8e
3; Mismatches
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99177B806671A85B
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4B4256A7496ABDED CRC64;
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                        Chloroplast.
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase
(EC 6.4.1.2) (ACCASE beta chain).
                                                   SEQUENCE
                                                                                                                                                                                 PIR; S66564; S66564.
InterPro; IPR000438; ACOACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryogenesis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elborough K.M.,
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MEDLINE=96207569; PubMed=8670092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Brassica.
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the multi-subunit form of acetyl-CoA carboxylase from Brassica napus
cloning and analysis of expression during oilseed rape
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                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THEM. J. 315:103-112(1996).
FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.
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                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long and this statement is not removed.
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                                                                                                               TIGR00515; accD;
                                                   489
                                                                 biosynthesis; Ligase; Zinc-finger; Chloroplast. 229 248 C4-TYPE (POTENTIAL)
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                                                55476 MW;
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    13.5%;
                                                                                                                                        TRASFF
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  Score 331.5;
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                                              4-TYPE (POTENTIAL)
540C79FB2A239432
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  DB
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core eudicots; Rosidae;
                                                CRC64;
Length 489;
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Best Local S
Matches 77
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Matches 76; Conserv
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                   InterPro; IPR000438; ACOACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.
-i- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Accession MG-20;
MEDLINE=21082929; PubMed=11214967;
Kato T., Kaneko T., Sato S., Nakam
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                                                             SEQUENCE
                                                                         Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast ZN_FING 235 257 C4-TYPE (POTENTIAL).
                                                                                                        TIGRFAMs; TIGR00515; accD;
                                                                                                                                                                               EMBL; AP002983; BAB33205.1;
                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                    between
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                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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77; Conserv
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                                                           501 AA;
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                                                           57038 MW;
             13.5%;
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Score 330.5; DB 1
Pred. No. 1.5e-12;
2; Mismatches 78
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0; Mismatches
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Best Local (
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PIR; S73119; S73119.
InterPro; IPR000438; ACOACC transfB.
InterPro; IPR000022; Carboxyl trans.
Pfam; PF01039; Carboxyl trans; I
PRINTS; PR01070; ACCTERPASEB;
TIGREAMS; TIGR00515; accD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Mol. Biol. Rep. 13:333-335(1995).
- PUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT INVOLVED IN CHARGAST CARBON METABOLISM.
- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-)
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Reith M.E., Munh
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Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
(EC 6.4.1.2) (ACCASE beta chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by ar
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                         QERLPAIILCASGGARMQEGMLSLMQMAKISSALEMHKKENLLYLSVLTSPTTGGVTASF
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                                                                                                                        YAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRAT
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                                                                                                                                                                                  13.4%;
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                                                                                                                                                               39;
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                                                                                                                                                            Score 329; DB
Pred. No. 9.7e
39; Mismatches
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.7e-13;
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RESULT 11
ACCD_TOBAC
ID ACCD_T
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete nucleotide sequence of the tobacco chloroplast genome: its gene organization and expression."; EMBO J. 5:2043-2049(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Bright Yellow 4;
Shinozaki K., Ohme M., Tanaka M., Wakasugi T.,
Shinozaki T., Zaita N., Chunwongse J., Oboka
Matsubayashi T., Zaita N., Chunwongse J., Oboka
Yamaguchi-Shinozaki K., Ohto C., Torazawa K., M
Deno H., Kamogashira T., Yamada K., Kusuda J.,
Tohdoh N., Shimada H., Sugiura M.;
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                           Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast.
ZN_FING 247 269 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                         InterPro; IPR000438; ACOACC_transfB.
InterPro; IPR000022; Carboxyl trans.
Pfam; PF01039; Carboxyl trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
TIGREAMS; TIGR00515; accD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z00044; CAA77362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCD OR YCF11 OR ZFPA.
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16-OCT-2001 (Rel.
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VAVILSDESELGGSLGTVASVRIMKAIHRATELKLELLVSPASGGARMQEDNRAFVMMVS 134
                                              IELLIDPGTWDPMDEDMVSLDPIEFHSEEEPYKDRIDSYQRKTGLTEAVQTGIGQLNGIP
                                                                                             IDSVLDPDSFISWNETP-----QYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIP
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                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12, Created)
12, Last sequence up
40, Last annotation
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                                                                                                                                         49;
                                                                                                                                       Score 326.5; DB 1;
Pred. No. 2.7e-12;
9; Mismatches 87;
                                                                                                                                                                                                                                       DFBC3312E6228868 CRC64;
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Torazawa K., Meng B.-Y.,
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VAIGVMDFQFMGGSMGSVVGEKITRLIEYAANQILPLIIVCASGGARMQEGSLSLMQMAK 400

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RESULT 12
RACCD ACCD
ACC P5676
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Best Local S
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                                                                                                                                                                                                                                                                                       InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
PF101039; Carboxyl_trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
TIGRPAMs; TIGR00515; accD; 1.
Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast.
ZN_FING 231 250 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000438; ACOACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20039611; PubMed=10574454;
Sato S., Nakamura Y., Kaneko T., Asamizu E., T
"Complete structure of the chloroplast genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress)
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28-FEB-2003 (Rel. 41, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase
(EC 6.4.1.2) (ACCASE beta chain).
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30-MAY-2000
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                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT CARBOXYLASE INVOLVED IN CHLOROPLAST CARBON METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                        262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATALYTIC ACTIVITY: ATP + acetyl-CoA + malonyl-CoA.
     72
                                                                                                         21
     GIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVM
                                                   IELSIDPG---TWNPMDEDMVSADPIKFHSKEEPYKNRIDSAQKTTGLTDAVQTGTGQLN
                                                                                                       IDSVLDPDSFISWN-----ETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6:283-290(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wurtele E.S., { (APR-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTVPEGSQAAEYLFQKGLFDLIVPRNLLKSVLSELFKL
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                                                                                                                                                                                                                                                                 488 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                              55609 MW;
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                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                     Score 324.5;
Pred. No. 3.
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                                                                                                                                                                                                                                                                 389B7C0B213A71CE CRC64;
                                                                                                                                                             Mismatches
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e of Arabidopsis
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                                                                                                                                                             Indels
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eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (EC 6.4.1.2) (ACCASE beta chain).
ACCD OR YCF11 OR ZFPA OR DEDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolfe K.H., Morden C.W., Palmer J.D.;
"Function and evolution of a minimal plastid genome f
"nonphotosynthetic parasitic plant.";
Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652(1992).
-!- FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT
INVOLVED IN CHLOROPLAST CARBON METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMs; TIGR00515; accD; 1.
Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast.
ZN_FING 235 257 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Asteridae; lamiids; Lamiales; Orobanchaceae; Orobancheae;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01039; Carboxyl trans; PRINTS; PR01070; ACCCTRFRASEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S78384; S78384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M81884; AAA65854.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- CATALYTIC ACTIVITY: ATP + acetyl-CoA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=93066301; PubMed=1332054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000438; ACOACC transfB. InterPro; IPR000022; Carboxyl trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4177;
                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                      Similarity 73; Conserv
  ITAAVQRHR-EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTG
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                                                    IAIGVMDFQFMGGSMGSVVGEKITRLIBYATNKILPLIIVCASGGARMQEGSLSLMQMAK
                                                                                                                                                                I EVLVDPDTWYPMDEDMSSLDPI BFHSEEEPYKDR I YSYQKRTGLTEAVQTGLGQLNGI P
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25, Last sequence up
40, Last annotation
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                                                                                                                                                                                                                                                                                                                          Score 323.5; DB 1;
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                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                               3.8e-12
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edons; core eudicots;
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PIR; S19230; BWFNZT.

InterPro; IPR000438; ACOACC transfB.

InterPro; IPR000022; Carboxyl trans.

Pfam; PP01039; Carboxyl trans; 1.

PRINTS; PR01070; ACCCTRERASEB.

TIGRPAMS; TIGR00515; accD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshinaga K., Kubota Y., Ishii T., Wada K., "Nucleotide sequence of atpB, rbcL, trnR, de genes from a fern Angiopteris lygodiifolia: Spermatophyta lineage before the separation Pteridophyta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast ZN_FING 51 73 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Mol. Biol. 18:79-82(1992).
-!- FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.
-!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Rosenstock;
MEDLINE=92119238; PubMed=1731980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
(BC 6.4.1.2) (ACCASE beta chain).
ACCD OR YCF11 OR ZFPA OR DEDB.
Angiopteris lygodiifolia (Turnip fern).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chloroplast
                                                                                                                                                                                                                                                                Local
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SSVSQIHQVQKKLLYIAVLTYPTTGGVTASFGMLGDIIIAEPKAYIAFAGKRVIEQTLRQ
                                   TAAVQRHR-EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGH
                                                                             ALGVMDFQSMGSSVVGEKITRLIEYATQESLPLIIVCASGGARMQEGTLSSMQMAKI
                                                                                                                   AVILSDESELGGSLGTVASVRIMKAIHRATELKLELLVSEASGGARMQEDNRAFVMMVSI
                                                                                                                                                         IELLIDRDTWIPMDEDMVAQDVLKFSDEDSYRNRISLSQKRTGLTDAVQTGIGNLNGTPV
                                                                                                                                                                                                   IDSVLDPDSFISWNETPQYDNL-----NQGYAETLERARSKAKCDESVITGEGTVEGIPV
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(Rel.
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46; Mismatches
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Pred. No. 2
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16-OCT-2001 (Rel.
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76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.
-!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ400848; CAB88738.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herrmann R.G., Mache R.;
"The plastid chromosome of spinach (Spinacia oleracea): complete nucleotide sequence and gene organization.";
Plant Mol. Biol. 45:307-315(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Geant d'hiver, and cv. I
MEDLINE=21187424; PubMed=11292076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE ACCD / PCCB
ELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKV
                                                                                MOMAKISSVLYDYOSNKKLFYVSILTSPTTGGVTASFGMLGDIIIAEPNAYIAFAGKRVI
                                                                                                                              VMMVSITAAVQRHREAHLPFLV-YLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVV 188
                                                                                                                                                                                 LNGIPVAIGVMDFQFMGGSMGSVVGBKITRLIEYASNKFIPLIIVCASGGARMQEGSLSL
                                                                                                                                                                                                                                  VEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAF 129
                                                                                                                                                                                                                                                                                     IELLIDPG----TWN---PMDDDMVSMDPIGFHSEEEAYKDRIDSYQIKTGLTEAVQTGIGQ
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40, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58907 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%; Score 321.5; DB 1
34.1%; Pred. No. 5.3e-12;
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http://www.isb-sib.ch/announce/
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Db 467 EQTLNKTVPEGSQAAEFLFHKGLFDPIVPRNLLKGVLSELFEL 509
Search completed: November 13, 2003, 06:41:00
Job time: 27 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: sp archea:*
2: sp bacteria
3: sp fungi:*
4: sp human:*
5: sp inverteb
6: sp mammal:*
7: sp mhc:*
8: sp organel:
9: sp phage:*
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12: sp virus:*
13: sp vertebr
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length: 2000000000
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2448
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sp_bacteria:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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        Q93kfl corynebacte
Q8fr58 corynebacte
Q9f6d6 streptomyce
Q910a1 streptomyce
Q910a1 streptomyce
Q8fxy7 brucella me
Q8fxy7 brucella su
Q98cm5 rhizobium 1
Q9gqg8 giardia lam
Q9gqd2 heliobacill
Q8yui2 anabaena sp
Q92tc7 rhizobium m
Q92tc7 rhizobium m
Q92tc7 rhizobiacte
Q8dia7 synechococc
Q25604 helicobacte
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0	08PJ30	16	295	u	338.5	5
O	Q8M9X6	œ	297	ω	339	44
Q8k633 streptococ	Q8K633	16	288		343	3
	Q8NZN5	16	288	4.	343	2
N	Q9CN12	16	304	4.	43.	41
Ψ	Q8NW59	16	285	4		0
	Q99TG2	16	285	4.	343.5	39
	Q8U9U5	16	317	14.1	344	38
	Q8D0U1	16	356	4.	45	37
	Q8ZD25	16	304	.4	45.	36
	дэлурэ	16	290	٠.	45.	35
	Q9K0D3	16	290	4	346.5	34
	Q8CS66	16	285	4.	54.	3
	Q9PJ00	16	280	4	355.5	32
	Q8XXY3	16	290	14.7	359	31
Q8dsp0 streptococ	Q8DSP0	16	288		360.5	30
Q9pka1 chlamydia	Q9PKA1	16	283	4	361	29
	Q9Z9C3	16	308	4	361.5	28
084295 ch	084295	16	308	4	361.5	27
œ	Q8UJA8	16	298	4	361.5	26
034571 bacillus su	034571	16	262	14.8	363	25
	Q8E1K1	16	291	4.	365	24
Q8e718 streptococc	Q8E718	16	291	4	365	23
Q8rga0 fusobacter	Q8RGA0	16	304	'n	367	22
Q9chf2 lactococcus	Q9CHF2	16	288	ŗ	368	21
O66754 aquife	066754	16	276		5	20
۳	Q9K841	16	282	ŗ	370.5	19
Q9rv15 deinococcus	Q9RV15	16	284	'n	72.	18
Q8ffh5 escherichi	Q8FFH5	16	332	ij	-	17

A CONTRACTOR OF THE CONTRACT O RESULT 1 Q93KF1 Query Match Best Local Similarity Matches 490; Conserv EMBL; AP005276; BAB98224.1; -. InterPro; IPR000438; ACOACC transfB. InterPro; IPR000022; Carboxyl trans. InterPro; IPR0001753; EnCOA hydrtse. Pfam; PF01039; Carboxyl_trans; 1. Pfam; PF00378; ECH; 1. PRINTS; PR01070; ACCCTRFRASEB. Ligase; Transferase; Complete proteome. Ligase; Transferase; Complete Proteome. SEQUENCE 491 AA; 52238 MW; 53D1B8757A92D82D CRC64; 093KF1 PRELIMINARY; PRT; 491 AA. 093KF1; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Putative carboxyltransferase subunit of acetyl-CoA carboxylase (Acetyl-CoA carboxylase beta subunit) (EC 6.4.1.2). ACCDA OR CGL0831. "Complete genomic sequence of Submitted (MAY-2002) to the EMBL; Y17592; CAC42827.1; SEQUENCE FROM N.A. STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025; Kim K., Peters-Wendisch Submitted (JUN-1998) to SEQUENCE FROM N.A. STRAIN=ATCC 13032; Corynebacterineae; NCBI_TaxID=1718; Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium. Nakagawa S.; Corynebacterium glutamicum (Brevibacterium flavum). 99.9%; P.G., Sahm H., Bikmanns B.J.; the EMBL/GenBank/DDBJ databases of Corynebacterium glutamicum e EMBL/GenBank/DDBJ databases. Score 2445; DB 16; Pred. No. 3.5e-138; 1; Mismatches 0; Length 491; ATCC 13032.";

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C STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

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C STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

C STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

A Kawarabayasi Y. Yamazaki J., Hino Y., Kikuchi H., Nakamura Y. A Kuchi M., Nakamura Y. A Kuchi M., Nakamura Y. Wamazaki M., Nishio Y., Sugimoto S.;

UR UBUG Y., Sugimoto S.;

C "The entire genomic sequence of Corynebacterium efficiens YS-XI Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; AP005217; BAC17717.1; -

DR EMBL; AP005217; BAC17717.1; -

DR EMBL; AP005217; BAC17717.1; -

C SEOUENCE 483 AA; 51545 MW; 653BA89519BBBDC7 CRC64;
                                                                                                        Query Match
Best Local S
Matches 302
                                                                                                                                                                                                                                                                                                                                                                                              Q8FR58; PRELIMINARY; PRT; 483 AA.
Q8FR58; O1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative carboxyltransferase subunit of acetyl-CoA
ACCDA OR CE0907.
                                                                                                                                                                                                                                                                                                                                     Corynebacterineae; Corynebacteriaceae; NCBI_TaxID=152794;
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Bacteria; Actinobacteridae; Actinomycetales;
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                                             MEHTSALTLIDSVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVE
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Pfam; PP03255; ACCA; 1.
Pfam; PP01039; Carboxyltrans; 1
PRINTS; PR01069; ACCCTRFRASEA.
PRINTS; PR01070; ACCCTRFRASEB.
TIGRFAMS; TIGR00515; accCj; 1.
SEQUENCE 578 AA; 60667 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20517899; PubMed=10931852;
Marti T., Hu Z., Pohl N.L., Shah A.N., Khosla C.;
"Cloning, Nucleotide Sequence, and Heterologous Expression of Biosynthetic Gene Cluster for R1128, a Non-steroidal Estrogen Antagonist. Insights into an Unusual Priming Mechanism.";
J. Biol. Chem. 275:33443-33448 (2000).
EMBL; AF293442; AAG30193.1; -.
InterPro; IPR001095; AC-COA_carboxylA.
InterPro; IPR000438; ACOACC transfB.
InterPro; IPR000438; ACOACC transfB.
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01-JUN-2002 (TrEMBLrel.
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Bacteria; Actinobacteria;
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NCBI_TaxID=140437;
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                                                   PLVVAAMDFAFLGGSLGGAVGELITLAAETALAEHLPLLIVSASGGARMQEGAVALMQMA
                                                                                                  PVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMV 133
                                                                                                                                                                                                    IDSVLDPDSFIS-WNETPQYDNLNQGYAET-----LERARSKAKCDESVITGEGTVEGI
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Last sequence update)
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                                                                                                                                                                                                                                                  Score 599.5; DB 2;
Pred. No. 7.9e-28;
'1; Mismatches 218;
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Submitted (Ar-
       STRAIN=A3(2) / M145;

MEDLINE=21996410; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Chandra G., Chen C.W., Collins

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor

Marren T., Wietzorrek A., Moodward J., Barrell B.G., Parkhill J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9L0A1
Q9L0A1;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                         Brown S.P.
Submitted
                                                                                                                                                                                       MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaire D.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed
the 8 Mb Streptomyces coelicolor A3(2) ch
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SCO2445 OR SCC24.16.
 Hopwood
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Streptomycineae; Streptomycetaceae; Streptomyces
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01-MAR-2003 (TrEMBLrel.
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Wicrobiol. 21:77-96(1996).
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(TremBirel 15, Last sequence update)
(TremBirel 23, Last annotation update)
tyl CoA carboxylase (Alpha and beta sub
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e EMBL/GenBank/DDBJ databases.
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Best Local S
Matches 138
                        SEQUENCE FROM N.A.

STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109, PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Rez Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson Selkov R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                        Brucellaceae; Bru
NCBI_TaxID=29459
                                                                                                                                                                    Bacteria; Proteobacteria;
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InterPro; IPR000438; ACOACC transfB
InterPro; IPR000022; Carboxyl trans
Pfam; PF01039; Carboxyl trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
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Nature 417:141-147(2002)
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lkorn R., Kyrpides N., (
genome sequence of the 
ella melitensis.";
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                                                                                                                                                         Brucella.
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                                                                                                                                                                    Alphaproteobacteria;
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annotation update)
rboxyl transferase
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., Reznik G.
              pathogen
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                                                    Goltsman
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                                        J.-J
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Best Local :
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Best Local
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Q8FXY7;
                                                                                                                                                                                                                                     STRAIN=1330 / Biovar 1;

MEDLINE=22247741; pubMed=12271122;

Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.

Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.

Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

"The Brucella suis genome reveals fundamental similarities between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000438; ACOACC trans:
InterPro; IPR000022; Carboxy1 tran
InterPro; IPR001202; WW Rsp5 WWP.
Pfam; PF01039; Carboxy1 trans; 1.
                                                                                                                                Brucella suis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TYEMBLrel. 23, Created)
01-MAR-2003 (TYEMBLE) 23, Last sequence update)
01-MAR-2003 (TYEMBLE) 23, Last annotation update)
01-MAR-2003 (TYEMBLE) 23, Last annotation update)
Accetyl-CoA carboxylase, carboxyl transferase, beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO0515; accD; 1.
PROSITE; PS01159; WW_DOMAIN_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                           animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                                                                                                                       Brucellaceae; Brucella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCD OR BR2107.
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B 301 AA; 33269 MW;
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 ELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMLGDIHIAEPGALIGFAGPRVIEQTIREKLPEGFQSSEYLMEHGMVDMVVSRLELKATI 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAV
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                             YIDRLKDYRSRTGMDDAIVNGLGTIEGLPIVATVQDFSFMGGSLGMGAGEAIIQGFEKAI
                                                         YAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRAT 105
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                                                                                        Conservative
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                                                                                                   17.6%;
43.3%;
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43.3%; Pred. No. 3.5e
tive 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Alphaproteobacteria;
                                                                                     ; Score 431.5; DB 1; Pred. No. 3.5e-18; 43; Mismatches 69
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                                                                                                                                                 BCB69B33AEA8D566 CRC64;
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RESULT 8
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Best Local
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InterPro; IPR000022; Carboxyl trans.
InterPro; IPR001002; WM_Rsp5_WMP.
InterPro; IPR001020; WM_Rsp5_WMP.
Pfam; PF01039; Carboxyl_trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kishida Y., Nakayama S., Nakazakı N., Surrege.
Mochizuki Y., Nakayama S., Nakazakı N., Tabeta S.;
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acetyl-CoA carboxylase carboxyltransferase beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRRAMS; TIGRO0515; accD; 1.

PROSITE; PS01159; WW DOMAIN 1; 1.

Transferase; Ligase; Complete proteome
SEQUENCE 308 AA; 34219 MW; 5FBE6E7/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q98CN5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q98CN5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLR5075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7:331-338 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                         FLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                        VLDPLKFRD-----EKRYTDRLKDAKAKTGLEDAIVNALGTIEGLPVVVTVQDFA
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                                                                                                                           ENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALPVMEAIARSRDPQ 263
                                                                                                                                                                                                                                                                                                                                         FMGGSLGMAAGDAIVHAFEVALQRKRPLILFAASGGARMQEGILSLMQLPRTTVGVDRLK
                                                                                                                                                                                                                                     <u>EAGLPYIVVLTNPTTGGVTASYAMLGDVHIAEPGALIGFAGPRVIEQTIREKLPDGFQRS</u>
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18,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 427; DB 16;
Pred. No. 6.6e-18;
6; Mismatches 87;
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PRELIMINARY;

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In the amitochondriate protist, Giardia lamblia,";

L Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF207740; AAG35712.1; -

R Interpro; IPR000195; AG-CoA CarboxylA.

R Interpro; IPR000438; ACOACC: TransfB.

R Interpro; IPR000498; Biotin_lipoyl.

R Interpro; IPR000089; Biotin_lipoyl.

R Interpro; IPR000081; Carboxyl trans.

R Interpro; IPR00081; Carboxyl trans.

R Interpro; IPR00081; PYC_OADA.

R Interpro; IPR003379; PYC_OADA.

R Pfam; PF00169; Carboxyl trans; 1.

R Pfam; PF00169; Carboxyl trans; 1.

R Pfam; PF00445; PYC_OADA; 1.
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Best Local (
Q8GDQ2
Q8GDQ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01069; ACCCTRFRASEA.
PRINTS; PR01070; ACCCTRFRASEB.
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Giardia lamblia (Giardia intestinalis)
Eukaryota; Diplomonadida; Hexamitidae;
NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9GQQ8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                           SPEGAASILOPSVYR--NNTAEMRANFISDAELLAHVQRCYPIDLRNAGVVNDIIVGPEY
                                                                                                                                                                                                          PPEGASAIL----FRDTNHAAEI----IERQGVQAHA-----LLSQGLIDGIVAETEH
                                                                                                                                                                                                                                                               SPEAEEOCOSRAISECLLAFOAVHVPIISIITGEGGSGGALALAGGNYVGILSKAFYNVI
                                                                                                                                                                                                                                                                                                         SQAAEELGIASSIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVYAAENAWLSAL
                                                                                                                                                                                                                                                                                                                                                                      GVFADTLPVIAIATSREDVLDPEAGLGSPTGYRFAARAIYLANRLSIPVITLVDTAGALP
                                                                                                                                                                                                                                                                                                                                                                                                                        ARIGGR-PVVLIGODRRFTLGPQE-----LRFARRGISLARELNLPIVSIIDTSGAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGAEVDTEDAFLVQDAFVYRDARNVTRPQPCDYLKNF-----VDMAASLRVDKCITVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGVALPVMEAI-----ARSRDPQRPGIGEIMETLGADVVKLSGARAGALSPAVRVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGFQTTDRAAATGAIDQLFDSLESAYASIHGILEVLIQRKGMQSVEAAAKTALLRLTGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGVQQAENLVKTGVIDGIVSPLQ-LRAAVAKTLKVI-----QPVEATD-----RFSPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIPVIVVIKDPCYGGTSGSFATLGDLTFGIKGSRFGFAGONVIKNTIFNGSNEAFDRSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLPFLVYLRNPTMGGAMASWGSSGHLTFABBGAQIGFLGBRVVELTT-----GHALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGSLGCAEGEKLSRACEYCVEHCMPLVIEAASGGVRMQEGVVALMQMANTTSCIESVKQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FINICSTDHMDFVFKGVSYKKQLEAARKATGSLCAMHVYHVKEPVEYIRA---VQEFAFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FISWNETPQYDNLNQG--YAETLERAR--SKAKCDESVITGEGTVEGIPVAVILSDFSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1338 AA;
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                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             z
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27.5%;
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Pred. No. 6.1e-16;
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 192;
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                         272
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RESULT 10
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Q8YUI2;
01-MAR-2002
                                                                                                   Watanabe A., Iriguchi M., Ishikav
Kishida Y., Kohara M., Matsumoto
Nakazaki N., Shimpo S., Sugimoto
Yasuda M., Tabata S.;
"Complete genomic sequence of the
                                     cyanobacterium Anabaena sp. DNA Res. 8:205-213(2001). EMBL; AP003589; BAB74063.1;
                                                                                                                                                                                      MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuri
Watanabe A., Iriguchi M., Ishikawa A.,
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01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
Acetyl-CoA carboxylase beta
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
                InterPro;
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"Whole-genome analysis of photosynthetic Science 298:1616-1620(2002).
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Sugimoto M.,
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A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont

"Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

R EMBL, AL591782; CAC41417.1; -.

R InterPro; IPR00002; Carboxyl_trans.

R FINITS; PR01039; Carboxyl_trans.

R FRINTS; PR01070; ACCCTRERASEB.
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Q92TC7;
01-DEC-2001
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Ligase; Complete proteome.
CEOMIENCE 304 AA; 33567 MW;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
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ACCD OR R00030 OR SMC02764.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                   ELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNDTMGGAMASW
     AEKCPLVMFPASGGARMQEGILSLMQLPRTTVALNMLKEAGLPYIVVLTNPTTGGVTASY
                                                                                                  YSDRLRDSRAKTELEDTIVAGLGQVQGIKLVAVAHEFNFIGGSLGIAAGEAIVKAFERAI
                                                                                                                                                        YAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRAT
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Pred. No. 7.9
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                       Q8DIE7 PRELIMINARY; PRT; 309 AA.
Q8DIE7;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acetyl-CoA carboxylase beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                     MQMAKTSAALNRLSEAKLPFISLLSDPTYGGVSASFAFLGDLIIAEPGAMIGFAGPRVIK
                                                                                                                                                                                                                                                                                                                                                                                                                               VMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVE
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                                                                                                                                                                                                                                                                                                                                 LTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVA-----
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39.6%;
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Pred. No. 1.
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Best Local S
Matches 94
                                                                  STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-P., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Nelson K., Quackenbush J., Dodson R., Khalak H.G., Glodek A.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Addams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21, Acetyl-CoA carboxylase beta
          pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Helicobacteraceae; Helicob
                                                                                                                                                                                                                                                                          Helicobacter pylori (Campylobacter pylori).
Helicobacter pylori (Epsilonproteobacteria;
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                                                            Venter J.C.
                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                 NCBI_TaxID=210;
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                                         "The complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura Y., Kaneko T., Sato S., Ikeuch
Watanabe A., Iriguchi M., Kawashima K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=B-1;
MEDLINE=22225144; PubMed=12240834;
MEDLINE=22225144; PubMed=12240834;
MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechococcus elongatus (Thermosynechococcus elongatus). Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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AE000604; AAD07995.1;
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AP005374; BAC09195.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATD
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                                                                                                                                                                                                                                                                    Helicobacter
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Last annotation update)
subunit (ACCD).
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Pred No. 1
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Tabata S.;
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Matches 87
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Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                                       Q50132;
Q50132;
01-NOV-1996
01-NOV-1996
01-MAR-2003
                                                                                                                                                                                 InterPro; IPR000438; ACOACC transtB.
InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
SEQUENCE 201 AA; 21323 MW; EF45B
                                                                                                                                                                                                                                       EMBL; U15184; AAA63045.1; -
InterPro; IPR000438; ACOACC
                                                                                                                                                                                                                                                               Robison K.;
Submitted (SEP-1994) to the
                                                                                                                                                                                                                                                                                                                Submitted (APR-1995)
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Smith D.R.;
                                                                                                                                                                                                                                                                                                                                                                         Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR00515; accD; 1. Hypothetical protein; Complete SEQUENCE 289 AA; 32553 MW;
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1769;
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InterPro; IPR000022; Carboxyl_
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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 118
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                                                                                                                                                       Similarity
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                                                          FLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRF
                                                                                                           MQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIG
                      SPT----TPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGALSPAVRVAL
                                                                                            MOEGTVAFLOMVKIAAAVKLSKRAGLPYLGYLKNPTTGGVFASWGSLGHVTVAEPGVLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLEHGLIDMIVHRKDLKKTLSDLIAMMTHKTSKI
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APPLICANT: Degussa-Hls AG APPLICANT: Porschungszentrum-Jlich GmbH ITITLE OF INVENTION: PROCESS FOR THE PREPARAT CURRENT APPLICATION UNMBER: US/09/362,899 CURRENT FILING DATE: 1999-07-29 EARLIER APPLICATION NUMBER: DE 19924365.4 EEARLIER FILING DATE: 1999-05-27 NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3 US-09-362-899-3 Query Match Best Local Simi Matches 491; GENERAL INFORMATION: TYPE: PRT ORGANISM: Corynebacterium glutamicum LENGTH: 491 Local Similarity \vdash VEKRFPTMVWGMEHTSALTLIDSVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCD 100.0%; ilarity 100.0%; Conservative C 0; Score 2448; DB 4; Pred. No. 3.5e-242; Mismatches 0; PREPARATION OF L-AMINO ACIDS Indels Length ٥, BY FERMENTATION Gaps AND

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Sequence 3, Application Patent No. 6361986

US/09362899

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acid
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C00.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SMITH, DOUGLAS
APPLICANT: MGO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                 125
                                                                                                                      172 TFAEPGAQIGFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKV 231
                                                                                                                                                                                112 LVSPASGGARMQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHL 171
                                                             232 IQPVEATDRFSPT----TPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAG 287
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ALSPAVRVALARIGGRPVVLIGQDRR 313
                                                                                                                                                          LVSPSSDGTRMQEGTVAFLQMVKIAAAVKLSKRAGLPYLGYLRNPTTGGVFASWGSLGHV 64
                               IADV---PKLIPTPQRPEPIPDVPAWNSVMGSRRPERPSVAQVLRHGATDRVLLSGPGHG 181
                                                                                             TVAEPGVLIGFLGPRVYELLYGEPFPSDIQTAENLQRHGVIDAIVTLDGLQLTLNRALTM 124
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600 ATLANTIC AVENUE
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                                                                                                                                                                                                                        ; Score 413; DB 4; Length 215; ; Pred. No. 3.9e-34; 29; Mismatches 75; Indels
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US-09-134-001C-3803
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SEQ ID NO 3803
LENGTH: 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
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                                                                                                                                                                                                           CITY: Waltham
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Sequence 3824, Application.
Sequence 3824, Application.
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Patent No. 6583275
Patent No. 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                             OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AKLDGIQYGVAVMDARFRMGSMGSVVGEKICRIIDYCTEHRLPFILFSASGGARMQEGII 183
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COUNTRY: USA
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Pred. No. 6.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and David Bush
AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORPORATION
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                                                                                                                                                                                    ; TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-5240
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                                                                                                                                                                                                                                                                                                                                      Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                Matches
                                                                                                                                                                                                                                                              SEQ ID NO 5240
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3824
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            LENGTH: 300
                                                                                                                                  Local
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NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 3824:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 ALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 FIIGVMDPNFIMGSMGTIVGEKITRLFERATKESLPVVLFTASGGARMQEGIFSLMQMAK 182
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 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 VAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 14.5%;
Similarity 35.5%;
                                                                                                                                Similarity
SFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRH 142
                                                                       SVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELPEDFQKAEFILSHGFVDQIVPRMELKQKIHTLLEL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIDEKSFEEWDTDLVTKDPLAFPE----YTEKIKKMQDKTGLHEAVLTGKATIQGIP
                                  SAKDPLKFVD-----SKPYPDRMREAQTKTGETEALIAMQGNLNGVDMIACAFEF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISAAVKRHSNEGLEYLTVLTDPTTGGVTASFAMEGDIILAEPQSLIGFAGRRVIEQTIKQ
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LOCATION: (B) LOCATION 1...289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 289 amino acids TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09328352
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                          13.5%; Score 331; DB 4; Length 300; 36.6%; Pred. No. 1.7e-25; tive 37; Mismatches 83; Indels
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Pred. No. 7e-28; Indels
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US-09-198-452A-76
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US-09-252-991A-28751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO 28751
; LENGTH: 339
; TYPE: PRT
                                                                   FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 76
LENGTH: 255
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              Sequence 76, Application US/09198452A Patent No. 6559294
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                                                                                                                                                                                                       TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and TITLE OF INVENTION: thereof and uses thereof, in particular full OF INVENTION: and treatment of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MARC J.
TITLE OF INVENTION:
TITLE OF INVENTION:
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                        APPLICANT: Griffais,
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TYPE: PRT ORGANISM: Chlamydia pneumoniae FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 LDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 13.5%; Score 329.5; DB Similarity 35.8%; Pred. No. 3e-25; 78; Conservative 39; Mismatches
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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US-08-973-275-1
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APPLICANT: KAMIYA, Shinj
APPLICANT: NAMBA, Kenryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: FINE MAGNETIC PARTICLES CONTAINING USEFUL PROTITILE OF INVENTION: BOUND THERETO, PROCESS FOR PRODUCING THE SAME, TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: JP 8-146833
EARLIER FILING DATE: 1996-05-16
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: PCT/JP97/01043
EARLIER FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: JP 8-97536
EARLIER FILING DATE: 1996-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/973,275B
CURRENT FILING DATE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Magnetospirillum AMB-1
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 317
TYPE: PRT
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LOCATION:
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les 75; Conserv
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NO. 595870/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 VFSLMQMVKTSAALAKLHEAGLPYISVLTNPTSGGVTASFAALGDIIIAEPKALICFAGP
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                               IVSIIDTSGAELSQAAEELGIASSIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADL
                                                                   EDEAIIGGLGRFRAASVMIIGHEKGHDTETRLKHNFGMAKPEGYRKAKRLMEMADHFQVP
                                                                                                    LSPAVRVALARIGGRPVVLIGQDR----RFTLG---PQELRFARRGISLARELNLP
                                                                                                                                      LR-----STYAKLTPWQKTQV-----ARHPERPHTLAYISTLIEDFTPLAGDRAFA
                                                                                                                                                                       LKVIQPVEATDRFSPTTPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGA
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IITLVDTAGAYPGVDÁÉARGQÁEAÍARSIETCLNVRVPLVSVÍÍGEGGSGGAIALATGNT 211
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                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                        Score 289; DB 2;
Pred. No. 3.8e-21;
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                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                          Length 317;
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US-09-328-352-8167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                  PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3786
LENGTH: 315
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             Sequence 3786, Apparent No. 63803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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LENGTH: 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AN
FILE REFERENCE: GTC99-03PA
                                                                                                                                                             FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                              APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: EPIDERMIDIS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                              PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 GALSPAVRVALARIGGRPVVLIGQDR-RFT------LGPQELRFARRGISLARELN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TEHFVEEILGTISNALSEL---DNNPERAGRDSRFTRF 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLDPERVMQNLKVVLKQALDELLPMDANERCEARYQRLMKF
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Pred. No. 6.2e-21;
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                                                                                                                                                                                                                                                   AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS DIAGNOSTICS AND THERAPEUTICS
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RESULT 11
US-09-107-532A-4837
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PATENT NO. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 84;
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Best Local Similarity
                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4837:
                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                         LENGTH: 262 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                          ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 AENAWLSALPPEGASAILFRDTNHAAEIIERQGVQAHALLSQGLIDGIV-----AETEH 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 AVRVALARIGGRPVVLIGQD------RRFTLG-PQELRFARRGISLARELNLPIVS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 | QPVEATDRESPTTPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGALSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENSTYSVISPEGAAALLWKDSNLAQIAAETMKITALDLLDLGIIDEVINEPLGGAQKDE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIDTKGAYPGKAAEERGQSESIAKNIMEMASLTVPVIAVVIGEGGSGGALGIGISNRVLM, 213
  ORGANISM: Enterococcus
                                                                                                                                                                                           TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                                                              TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUT
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection FILE REPRENCE: 9710-003-999 CURRENT FILE REPRENCE: 9710-003-999 CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 433, Application Patent No. 6559294
GENERAL INFORMATION:
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304 FIIQEWLRLKDLAIEEL--
                                                                                                                    410 PPEGASAILFRDTNHAAEIIERQGVQAHALLSQGLIDGIVAE-----
                                                                                                                                                                                                                                                                                     301 GGRPVVLIGQD------RRF-TLGPQELRFARRGISLARELNLPIVSIIDTSGAEL 349
                                     454 HFVEEILGTISNALSELDNNPERAGRDSRFTRFERL 489
                                                                                                                                                                184 GLTAEERGOGWAIAKNLFELSRLATPVIIVVIGEGCSGGALGMAVGDSVAMLEHSYYSVI 243
                                                                                                                                                                                                      350 SQAAEELGIASSIARTISKLIDAPLPTVSVIIGQGVGGGALAMLPADLVYAAENAWLSAL 409
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                                                                               SPEGCASILWKDPKKNSEAASMLKWHGENLKQFGIIDTVIKEPIGGAHHDPALVYSNVRE
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(B) LOCATION
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Pred. No. 1.1e-18;
40; Mismatches 114;
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US-08-611-107-12
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE TENGTH: 327 amino acids
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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5801,
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                                                                      340 SIIDTSGAELSQAAEELGIASSIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVY 399
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AAENAWLSALPPEGASAILFRDTNHAAEIIERQGVQAHALLSQGLIDGIVA------
                                  TFIDTPGAYAGVSAEELGQGEAIAVNLREMFRFSVPILCTVIGEGGSGGALGIGVGDRLL
                                                                                                            LALVGGVGALDGQPVVFLGHQKGRDTKDNVLRNFGMASPGGYRKALRLMEHADRFGMPIL
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25.2%; Pred. No. 2.2
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US-08-422-560A-12
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Patent No. 5910626
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 86; Conserv
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INFORMATION FOR SEQ ID NO:
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 0
FILING DATE: 02-OCT-1992
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 14-APR-199
CLASSIFICATION: 800
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LENGTH: 327 amino acids
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                        340 SIIDTSGAELSQAAEELGIASSIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVY 399
                                                                                                                                                  291 PAVRVALARIGGRPVVLIGQD------RRFTL-GPQELRFARRGISLARELNLPIV 339
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400 AAENAWLSALPPEGASAILFROTNHAAEIIERQGVQAHALLSQGLIDGIVA---
                                                                                                                                                                                                                          231 VIQPVEATDRFSPTTPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGALS 290
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                                                                                                             LALVGGVGALDGOPVVFLGHOKGRDTKDNVLRNFGMASPGGYRKALRLMEHADRFGMPIL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                     TFIDTPGAYAGVSAEELGQGEAIAVNLREMFRFSVPILCTVIGEGGSGGALGIGVGDRLL 221
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                                                                                                                                                                                       -----REIFSNLSPAQRIQV-----ARHPRRPSTLDYIQAISDEWIELHGDRNGSDD 101
                                                                                                                                                                                                                                                                 LEFEKPLVE---LEERITQIRT-----LAADNQVD---VSGQIQQLEARAIQLR---
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Gornicki, Piotr
                                                                                                                                                                                                                                                                                                                                           Conservative
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02-OCT-1992
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METHODS FOR
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2; Mismatches 138;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USE
                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                           Indels 55;
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; LENGTH: 327 amino
; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
US-08-468-793-12
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US-08-468-793-12
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Best Local Similarity
Matches 86; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 30-SEP-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
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APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (512) 418-301
TELEFAX: (713) 789-2679
TELEX: 79-0924
TELEX: 79-0924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US SN 07/956,700 FILING DATE: 02-OCT-1992 CLASSIFICATION: 800
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291 PAVRVALARIGGRPVVLIGQD---
                                                                                                                                              231 VIQPVEATDRESPTTPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGALS
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                                                                     -----REIFSNLSPAORIOV-----ARHPRRPSTLDYIQAISDEWIELHGDRNGSDD 101
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linear
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                                                                                                                                                                                                                                                                                                                                                                   10.3%; Score 252.5; DB 3; 25.2%; Pred. No. 2.2e-17; tive 62; Mismatches 138;
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                                                                                                                                                             340 SIIDTSGAELSQAAEELGIASSIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVY 399
                                                                                                                                                                                              AAENAWLSALPPEGASAILFRDTNHAAEIIERQGVQAHALLSQGLIDGIVA------
                                                             MFEHSVYTVASPEACASILWRDAGKAAQAAEALKITARDLKQLGILDEIITEPLGGAHSA 281
PLETAQSLRQVL---LRHLKDLQALSPAQLREQRYQKFRQL 319
                              --ETEHFVEEILGTISNALSELDNNPERAGRDSRFTRFERL 489
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Search completed: November 13, 2003, 06:58:22 Job time : $32\ \text{secs}$

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Perfect score:
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                                         368
343.5
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Match Length
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/2/pūbpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pūbpaa/US06_PUBCOMB.pep:*
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10 US-09-738-626-4429
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15 US-10-156-761-13252
10-09-815-242-11385
10 US-09-815-242-13952
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Sequence 3, Appli
Sequence 181, Ap
Sequence 181, Ap
Sequence 18252, A
Sequence 10925, A
Sequence 10925, A
Sequence 11385, A
Sequence 11385, A
Sequence 11212, A
Sequence 11212, A
Sequence 11212, A
Sequence 12618, A
Sequence 13618, A
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4. U	44	43	42	41	40	39	38	37	36	ა 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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7.8	7.8	8. 5	8.8	8.9	8.9	9.8	10.2	10.3	10.3	10.4	10.5	10.5	10.7	10.7	10.8	10.8	10.9	11.0	11.0	11.0	11.0	11.0	11.2	11.2	11.3	11.6	11.7	11.8	11.9
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US-10-205-823-254	US-10-224-539A-10	-10-259	-09-738-62	4-53	US-10-156-761-11401	US-09-738-626-4284	US-09-815-242-11934	US-09-767-479-12	US-09-841-132-566	-66	-1151	9-815-242-1133	m	US-09-925-301-1140	09-815-242-	-132-	9-8	US-10-156-761-9840	US-09-815-242-13619	US-09-815-242-13366	09-815	9-815-242	US-10-187-267A-47	US-09-815-242-12908	09-815-242-58	045-612#	-10-156-761	US-09-815-242-11014	US-10-156-761-10868
e 25	e 10,	e 2,	42		Sequence 11401, A	O	119		566, Ar	e 666!	Sequence 11511, A	11339	e 589	1140	1092	496,	1004	ce 9841	1361	1336	1389	4964	ce 47,	1290	5892	e 31,	e 10240,	\vdash	Sequence 10868, A

ALIGNMENTS

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                                                                                                                                                                                                      ; LENGTH: 491
TYPE; PRT
; ORGANISM: Corynebacterium glutamicum
US-10-024-370-3
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US-10-024-370-3
                                                                                                                            Query Match 100.0%; Score 2448; DB 14; Best Local Similarity 100.0%; Pred. No. 1.1e-217; Matches 491; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10024370 Publication No. US20020142405A1
                                                                                                                                                                                                                                                                                                                                APPLICANT: MOCKEL, BETTINA
TITLE OF INVENTION: PERCESS FOR THE PREPARATION OF L-AMINO ACIDS BY
TITLE OF INVENTION: PERCENTATION AND NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: accDA GENE
TITLE OF INVENTION: accDA GENE
TITLE REPERENCE: 21123-284139-MAS
CURRENT FAPLICATION NUMBER: US/10/024,370
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/362,899
PRIOR PILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 3
                      61
                                                     ESVITGEGTVEGIPVAVILSDPSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGA .120
                                                                                                                                 Indels
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                                                                                                                                                                                                                ; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-4429
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US-09-738-626-4429
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALENTIN VEX: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4429, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     SEQ ID NO 4429
LENGTH: 491
                                                                                                                                   Matches 490;
                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                        Local Similarity
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                ESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGA 120
                                                   MEKRFPTMVWGMEHTSALTLIDSVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCD
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TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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Pred. No. 2e-217;
1; Mismatches
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                                                                      ; TYPE: PRT ; ORGANISM: Mycobacterium tuberculosis US-09-712-363-181
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CURRENT APPLICATION NUMBER: US/09/712,363

CURRENT FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: PCT/US00/02246

PRIOR FILING DATE: 2000-01-28

PRIOR PELICATION NUMBER: 60/179,531

PRIOR FILING DATE: 2000-02-01

PRIOR APPLICATION NUMBER: 60/117,844

PRIOR APPLICATION NUMBER: 60/117,844

PRIOR APPLICATION NUMBER: 60/117,844

PRIOR APPLICATION NUMBER: 60/118,206,

PRIOR APPLICATION NUMBER: 60/126,593

PRIOR PILING DATE: 1999-03-06

PRIOR APPLICATION NUMBER: 60/126,593

PRIOR APPLICATION NUMBER: 60/126,593

PRIOR APPLICATION NUMBER: 60/134,093

PRIOR APPLICATION NUMBER: 60/134,093
                                                                                                                                                                                                             PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR PPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                  NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSEQ for Win
SEQ ID NO 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 181, App
Patent No. US2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rotetein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Eisenberg, David
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20020164588A1
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              42.8%;
                                                                                                                                                                          Version
              Score 1047; DB 10;
Pred. No. 4.5e-88;
                                Length 495;
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                                                                                                                                        ; LENGTH: 465
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13252
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-82
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JF 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13252, Application US/10156761 Publication No. US20030119018A1
                                                                      Matches
                                                                                                      Query Match
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                                                                                        Local
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                                                                                      Similarity
                 LTLIDSVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAV
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 LPVAEGAYAPDGPLSW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGSTVGPAALREARRGMALAAELCLPLVLVIDAAGPALSAAAEQGGLAGQIAHCLAELVI
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                                                                      Conservative
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                                                                19.9%; Score 487.5; DB 15; Lengtl 29.9%; Pred. No. 2.4e-36; tive 66; Mismatches 208; Indels
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OGYDASRARATERTGEDESVVCGRARIDGTPAVL 70
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                                                                                                  Length
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; ORGANISM: Enterococcus
US-09-815-242-10925
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Query Match 16.3%; Score 400; DB 9; Length 288; Best Local Similarity 42.6%; Pred. No. 1.4e-28; Matches 89; Conservative 39; Mismatches 79; Indels
                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10925
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                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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LENGTH: 289
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                                                                                                                                                                                                                                              Query Match
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PRIOR
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PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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 195
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                              146 HLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQAEN 205
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                                                                                                       GGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHREA 145
 KLPFISLLSDPTYGGVSASFAFLGDLIIAEPGAMIGFAGPRVIKQTIGADLPEGFQTAEF
                                                                     GGSLGSVEGEKIVRAINRAVAKREALLIVSASGGARMQESTYSLMQMAKTSAALNRLSEA
                                                                                                                                        DPLNFVD-----KESYKQRIKKYEKRTNRPSSVISGEAKINRMPLQIVVFDFSFM
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Zyskind, Judith W.
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Xu, H. Howard
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Pred. No. 4.3e-27;
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US-09-815-242-13952
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 98
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13952, Application US/09815242 Patent No. US20020061569A1
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Best Local :
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                         FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                     APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel H
TITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/895,913A
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TYPE: PRT
ORGANISM: Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 LVKTGVIDGIVSPLQLRAAVA-----KTLKV 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 DPLNFVD-----KESYKORIKKYEKRINRPSSVISGEAKINRMPLQIVVFDFSFM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 DPDSFISWNETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFSFL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
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Pred. No. 4.3e-27;
0; Mismatches 72;
                                                                                                                                                                   Essential Genes
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
ITITLE OF INVENTION: Identification of Essential Genes in
ITITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,731
PRIOR APPLICATION NUMBER: 60/253,625
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US-09-815-242-10230
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US-09-815-242-13952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10230, Application Patent No. US20020061569A1
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Best Local Similarity
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                    APPLICATION NUMBER: 60/269,308
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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DATE:
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; ORGANISM: Haemophilus influenzae US-09-815-242-11212
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PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11212
                                           Query Match
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10230
LENGTH: 304
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APPLICANT:
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APPLICANT:
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Best Local Similarity
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                                                                                                              LENGTH: 296
TYPE: PRT
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  Local Similarity hes 81; Conserv
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Yamamoto, Robert
Xu, H. Howard
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    Conservative
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15.0%; Score 368; DB 9; Length 296; 36.8%; Pred. No. 1.3e-25; rative 45; Mismatches 80; Indels
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US-09-815-242-12618
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Best Local
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus aureus
-09-815-242-12618
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 285
                                                                                                                                                                                                                                                              Local Similarity
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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176
                                   128 AFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRV 187
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                                                                                                                                                                                                 13 EHTSALTL---IDSVLDPDSFISWNETPQYDN-LN-QGYAETLERARSKAKCDESVITGE
                                                                                                                                                                                                                                         82;
                                                                                                      GTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNR 127
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                                                                                                                                                          DHHIALTAYKRIEAISDEGSFTEFDKGMTSANPLDFPSYIEKIEKDQQKTGLKEAVVTGT
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SLMOMGKTSVSLKRHSDAGLLYISYLTHPTTGGVSASFASVGDINLSEPKALIGFAGRRV
                                                                             AQLDGMKFGVAVMDSRFRMGSMGSVIGEKICRIIDYCTENRLPFILFSASGGARMQEGII
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Trawick, John D.
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Zyskind, Judith W.
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RESULT 13
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US-09-815-242-5424
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FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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LENGTH: 252
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Best Local Similarity
Matches 81; Conserv
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-11-27
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                                                                                                      207
                                                                                                                                                                                                                                                   128 AFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRV 187
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                                                                                                                                                  VELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQ 233
                                                                                                                                                                                                     SLMOMGKTSVSLKRHSDAGLLYISYLTHPTTGGVSASFASVGDINLSEPKALIGFAGRRV
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                                                                                                   IEQTINEKLPDDFQTAEFLLEHGQLDKVVHRNDMRQTLSEILKIHQ
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Trawick, John D.
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Sequence 13365, Application U Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.

Application US/09815242

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US-09-815-242-13618
; Sequence 13618, Application US/09815242
; Patent No. US20020061569A1
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                   APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essen
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                 APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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SEQ ID NO 13365
LENGTH: 288
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Best Local (
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILLING DATE: 2001-03-1
PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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73; Conserv
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39.0%; Pred. No. 1.8e-22;
ative 36; Mismatches 78;
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                                                                                                                 of Essential Genes
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                                    PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
              APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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US-09-815-242-11898
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PRIOR FILLING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/243,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                Sequence 11898, Application US/09815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
                                                                                                        APPLICANT:
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APPLICATION NUMBER: 60/269,308
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Zyskind, Judith W.
                                                                                                      Carr, Grant
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6; Mismatches 78;
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